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New polynucleotide encoding flavonoid biosynthetic enzymes for creating transgenic plants and for immunological screening of cDNA libraries
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Compugen Ltd.
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                                                            AAY96583-87 are (partial) isoflavone O-methyltransferases isolated from various soybean (Glycine max) tissues. cDNA libraries Se4, Sr1, SrrIc and sellc were prepared from soybean embryo (19 days after flowering), root, 8-day old root and seed (25 days after flowering).

Isoflavone O-methyltransferase catalyses the first step in degradation of daidzein Suppression of this enzyme will yield higher concentrations of this beneficial isoflavone in, e.g. soybean seed. Flavonoids serve as co-pigments in flower colour, stimulate pollen tube growth, attract pollenators, act as feeding deterrents and protect against UV irradiation in fruits and seeds. The cDNA and proteins can be used to isolate homologues, for immunological screening and for positive
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ive 0; Mismatches 0;
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                        Claim 10; Page 32-33; 39pp; English.
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AAV96583-87 are (partial) isoflavone O-methyltransferases isolated from various soybean (Glycine max) tissues. CDNA libraries se4, sr1, srr1c and self twere prepared from soybean embryo (19 days after flowering).

Isoflavone O-methyltransferase catalyses the first step in degradation of daidacein. Suppression of this enzyme will yield higher concentrations of this beneficial isoflavone in, e.g. soybean seed. Plavonoids serve as Co-pigments in flower colour, stimulate pollen tube growth, attract pollenations in fruits and seeds. The CDNA and proteins can be used to insolate homologues, for immunological screening and for positive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 YFLEPNCQGAMNQLKRWVHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAFRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFV 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 GGDMFKCIPKADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKD 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGDMFNSIPQADAVLLKWVLHNWTDENCIKILQKCRDSISSKGNSGKVIIIDAVINBKLD 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57
                                                                                                                                                               New polynucleotide encoding flavonoid biosynthetic enzymes for creating transgenic plants and for immunological screening of cDNA libraries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 350;
                                                   Falco SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.7%; Score 1012; DB 21; 54.9%; Pred. No. 2.4e-97;
                                                   Fader GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycine max isoflavone O-methyltransferase
(DUPO ) DU PONT DE NEMOURS & CO E I.
                                                 odell JT,
                                                                                                                                                                                                                                    Claim 10; Page 37-39; 39pp; English
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Best Local Similarity 54.9%
Matches 196; Conservative
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                                         Famodu OO, McGonigle B,
                                                                                          2000-442680/38
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(first entry)

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Glycine max partial isoflavone O-methyltransferase.
      26-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAFRDCNWVFBGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFV 241
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                                                                                                                                                                                                                                                                     AAY96583-87 are (partial) isoflavone O-methyltransferases isolated from various soybean (Glycine max) tissues. cDNA libraries se4, sr1, srr1c and sellc were prepared from soybean embryo (19 days after flowering), root, 8-day old root and seed (25 days after flowering).

Isoflavone O-methyltransferase catalyses the first step in degradation of daidzein. Suppression of this enzyme will yield higher concentrations of this beneficial isoflavone in, e.g. soybean seed. Flavonoids serve as co-pigments in flower colour, stimulate pollen tube growth, attract pollenators, act as feeding deterrents and protect against UV irradiation in fruits and seeds. The cDNA and proteins can be used to insolate homologues, for immunological screening and for positive
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                                                                                                                                                                                                              New polynucleotide encoding flavonoid biosynthetic enzymes for creating transgenic plants and for immunological screening of cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 BRQVTELKLIMDVHMACIINGKERKEEDWKKLFMRAGFQSYKISPFTGYLSLIEIYP 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ASWIN-QKEIELFEGQSILYMQLYGHLRPMCLKWAVQLGIPDIIQNHA--KPIELSDLVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 351;
                                                                                                                                                          SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                          Falco
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 53.7%; Score 1012; DB 21; Best Local Similarity 54.9%; Pred. No. 2.4e-97; Matches 196; Conservative 69; Mismatches 84;
              /note= "Encoded by GAAGATCATGAA"
                                                                                                                                                          Fader GM,
                                                                                                                                                       McGonigle B, Odell JT,
                                                                                                                                (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                 Claim 10; Page 34-35; 39pp; English.
                                                                                   99WO-US30338
                                                                                                         98US-0113190.
                                                                                                                                                                             WPI; 2000-442680/38
Misc-difference 90
                                                                                                                                                                                                                                                                                                                                                                                                                                351 AA;
                                                                                                                                                                                                                                                                                                                                                                                                          selection methods.
                                                                                                                                                                                          N-PSDB; AAA29323
                                   WO200037656-A2
                                                                                  20-DEC-1999;
                                                                                                         21-DEC-1998;
                                                           29-JUN-2000
                                                                                                                                                       Famodu 00,
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AAY96583-87 are (partial) isoflavone O-methyltransferases isolated from various soybean (Glycine max) tissues. CDNA libraries se4, sr1, srrlc and sellc were prepared from soybean embryo (19 days after flowering), root, 9 day old root and seed (25 days after flowering).

Isoflavone O-methyltransferase catalyses the first step in odgradation of daidzein. Suppression of this enzyme will yield higher concentrations of this beneficial isoflavone in, e.g. soybean seed. Flavonoids serve as co-pigments in flower colour, stimulate pollen tube growth, attract pollentors, act as feeding deterrents and protect against uv irradiation in fruits and seeds. The CDNA and proteins can be used to insolate homologues, for immunological screening and for positive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotide encoding flavonoid biosynthetic enzymes for creating transgenic plants and for immunological screening of cDNA libraries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 RKASEIFQGQALLYXHLLGFIDSKCLKWMVELDIPDIIHSHSHGQPITFSELVSILQVPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CIPKADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 LMTTYHHFGEWIRGEDPTVHBTAFGTSFWGLLEKNPTOMSLFNEAMASDSRAVDLALKNC
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O-methyltransferase; soybean; degradation; daidzein; flower colour; growth; pollination; irradiation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Falco
                                                                                                                                                                                                                                                                                                                                                                                                                                 Fader GM,
                                                                                                                                                                                                                                                                                                                                                                           Ξ.
                                                                                                                                                                                                                                                                                                                                                                                                                              odell JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 10; Page 35-36; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                     (DUPO ) DU PONT DE NEMOURS & CO
                                                                                                                                                                                                                                                          99WO-US30338
                                                                                                                                                                                                                                                                                                               98US-0113190
                                                                                                                                                                                                                                                                                                                                                                                                                              McGonigle B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-442680/38
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Matches 192: Connection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 348 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAA29324
                                                                                                                                            WO200037656-A2
                                                                                                                                                                                                                                                          20-DEC-1999;
                                                                                                                                                                                                                                                                                                               21-DEC-1998;
                                                                                      Slycine max.
                                                                                                                                                                                                    29-JUN-2000
Isoflavone
Flavonoid;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Famodu 00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239
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187 178

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AAY96586 standard; Protein; 348

AAY96586;

AAY96586 ID AAY9 XX AC AAY9 XX

28

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248 MKCILHDWDDKECIEILKRCKEAV--PVKGGKVIIVDIVLNV-QSEHPYTKMRLTLDLDM 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 MRYLAHNGFFEIVRIHDNIBAYALTAASELLVKSSELSLAPMVEYFLEPNCOGAWNOLKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 GLSGESGTAFEKALGTNIWGYMAEHPEKNOLFNEAMANDSRLIMSALVKECGNIFNGITT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 MRYLVHMKLFTKASIDGELR-YGLAPPAKYLVKGWDKCMVGSILAITDKDFMAPWHYLKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 WVHEEDLIVFEVSLGIPFWDFINKDPAYNKSFNEAMACDSQMLNLAF-RDCNWVFEGLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 IVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QALLYKHLIGFIDSKCLKMMVELDIPDIIHSHSHGQPITFSELVSILQVPPTKTRQVQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 QAKLWNFIYGFAESLVLKCAVQLDLANII--HNSGTSMTLSELSSRLPSQPVNEDALYRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257 LKLVLHNWNDNDCMKILENCKEAISGESKIGKVVVIDTVINENKDERQVTELKLLMDVHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents norcoclaurine 6-0-methyltransferase (6-0MT), Also described is a method for the preparation of the secon metabolite of a plant derived from coclaurine or reticuline.
                     TELKLIMDVHMACIINGKERKEEDWKKLFMEAGFQSYKISPFTGYLSLIEIYP 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New norcoclaurine 6-0-methyl-transferase - useful for preparation
                                      TRIKLSLDIVMS-TWNGRERSEKEWKQMFIEAGFKHCKIFPIFGFRSLIELYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 347;
                                                                                                                                                                                                                                                      Coptis japonica; norcoclaurine 6-0-methyltransferase; 6-0MT; secondary metabolite; coclaurine; reticuline.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 33.7%; Score 636.5; DB 20; Length Local Similarity 38.9%; Pred. No. 7.3e-58; es 133; Conservative 70; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         305 MLNIGGKERIBEEWKKLIHDAGYKGHKITQITAVQSVIEAYP 346
                                                                                                                                                                                                                          Coptis japonica norcoclaurine 6-0-methyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317 ACIINGKERKEEDWKKLFMEAGFQSYKISPFTGYLSLIEIYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MITC ) MITSUI PETROCHEM IND CO LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 11-12; 27pp; Japanese
                                                                                                                               Ā
                                                                                                                               Protein; 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secondary plant metabolite
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                                                                                                                              AAY24396 standard;
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                                                                                                                                                             AAY24396;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY96583-87 are (partial) isoflavone O-methyltransferases isolated from various soybean (Glycine max) tissues. CDNA libraries se4, sr1, srr1c and ss1c were prepared from soybean embryo (19 days after flowering).

1 soflavone O-methyltransferase catalyses the first step in degradation of daidzein Suppression of this enzyme will yield higher concentrations of this beneficial isoflavone in, e.g. soybean seed. Plavonoids serve as pollemators, act as feeding deterrents and proteins cup irradiation in fruits and seeds. The object against UV irradiation in fruits and seeds. The object and for positive isolate homologues, for immunological screening and for positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPTKTRQVQSLMRYLAHNGFFEIVRIHDNIE-AYALTAASELLVKSSELSLAPMVEYFLE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FKCI PKADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQV 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PNCQGAMNQLKRWVHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFR 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide encoding flavonoid biosynthetic enzymes for creating transgenic plants and for immunological screening of cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLLMTTYHHFGEWIRGEDPTVHETAFGTSFWGLLEKNPTOMSLFNEAMASDSRWVDLALK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 NGRKASEIFQGQALLYKHLLGFIDSKCLKMMVELDIPDIIHSHSHGQPITFSELVSILQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                        daidzein;
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                                                                                                                                                     Isoflavone O-methyltransferase; soybean; degradation; daid:
Flavonoid; flower colour; growth; pollination; irradiation
                                                                                                                                                                                                                                                                                                                                                                                           sc;
                                                                                                                                                                                                                                                                                                                                                                                           Falco
                                                                                                                         Glycine max partial isoflavone O-methyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                           Fader GM,
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Н
                                                                                                                                                                                                                                                                                                                                                                                       Odell JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 10; Page 30-31; 39pp; English.
                                AAY96583 standard; Protein; 350 AA.
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                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-442680/38.
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Best Local Similarity
Matches 191; Conserv
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                                                                                                                                                                                                                                                                                                                             21-DEC-1998;
                                                                                                                                                                                                                                                                                                20-DEC-1999;
                                                                                          26-SEP-2000
                                                                                                                                                                                                     Glycine max
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                                                             AAY96583;
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RESULT 5
              AAY96583
ID AAY
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128 ATLAPFVSLALQPIAACPHALG-ISAWFRQEQHEPSPYGLAFRQTPTIWEHADD----VNA 183
                                                                                                                         227 NVVENLSGSNNLTFVGGDMFKCIPKADAVLLKLVLHNWNDNDCMKILENCKEAISGESKT 286
                                                                                                                                                                                                                                         244 HVVAGAPSDGNVQFVAGNNFESIPPATAVFLKKTLHDWGDDECVKILKNCKQAISPRDAG 303
                                                                                                                                                                                                                                                                                              287 GKVVVIDTVINENKDERQVTELKLLMDVHMACIINGKERKEEDWKKLFMEAGFQSYKISP 346
                                                                                                                                                                                                                                                                                                                            This represents a polypeptide having the enzymatic activity of (8)-3'-hydroxy-N-methylcoclaurine 4'-O-methyltransferase (4'-OWT). A vector containing the DNA can be used to transform a microbe for the recombinant preparation of the enzyme. The enzyme can be used to prepare a secondary metabolite of a plant derived from reticuline which is useful as a raw
114 LSLAPMVEYFLEP--NCOGAWNQLKRWVHEEDLTVFEVSLG---TP-FWDFINKDPAYNK 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 SLMRYLAHNGFFEIVRIHDNIEAYALTAASELLVKSSELSLAPMVEYFLEPNCQGAWNQL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 KAQAHVWKIIYGFADSLVLRCAVELGIVDIIDNNN--QPMALADLASKLPVSDVNCDNLY 70
                                                                                                168 SFNEAMACDSO-MINLAFRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 QGQALLYKHLIGFIDSKCLKWMVELDIPDIIHSHSHGQPITFSELVSILQVPPTKTRQVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S)-3'-hydroxy-N-methylcoclaurine 4'-O-methyltransferase (4'-OMT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (S)-3'-hydroxy-N-methylcoclaurine 4'-O-methyltransferase; 4'-OMT; enzyme; secondary metabolite; reticuline; drug.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New (S)-3'-hydroxy-N-methylcoclaurine 4'-O-methyltransferase gene encoding it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 580.5; DB 20; Length ; Pred. No. 5.8e-52; 83; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MITC ) MITSUI PETROCHEM IND CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY27183 standard; Protein; 350 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                     363 VIGDVSVIIEVYP 375
                                                                                                                                                                                                                                                                                                                                                                                         347 FTGYLS-LIEIYP 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 LRALRRLMRVLTVTGIFSVVEQPPAGGGDDSTVHTSDDEAVVVYRLTAASRFLVSDDVST 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a caffeic O-methyltransferase, encoded by a cDNA clone (see AAX25200) isolated from a line A643 cDNA library. The invention provides methods and compositions relating to altering lignin biosynthesis and composition of plants. Isolated nucleic acids (see AAX25196-216) that code for plants. Isolated nucleic acids (see AAX25196-216) that code for colling (see AAY05657-77) involved in lignin biosynthesis are claimed. Also claimed are recombinant expression cassettes, host cells (especially maize or sorghum), and transgenic plants and seeds. The claimed nucleic acids can be used to transform a plant to modulate lignin biosynthesis. A claimed method involves transforming a plant cell with a recombinant expression cassette comprising a lignin biosynthesis polynucleotide operably linked to a promoter, growing the plant cell under plant growing conditions, and inducing expression of the polynucleotide for a time sufficient to modulate (preferably increase) lignin biosynthesis in the plant. The plant lignins can be used as a fuel source, immunestial of increased lignin content can be used as a fuel source, immunestial of increased lignin content can be used as a fuel source, immunestial of increased lignin content can be used as a fuel source, immunestial of increased lignin content can be used as a fuel source, immunestial of increased lignin content can be used as a fuel source, immunestial of increased lignin content can be used as a fuel source, immunestial case and in the pulp and paper industry.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 SQDLLQAHDELLHHSLCFAKSLALAVALDLRIPDAIHHHGAG-GATLLQILAETALHPSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 31; Gaps
                                                                                                                                                                                                                                    Maize; corn; caffeic O-methyltransferase; lignin; transgenic plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding plant lignin biosynthesis enzymes - used to transform plants to modulate lignin biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 20; Length 375;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and in the pulp and paper industry. Decrea improves the digestibility of fodder crops.
                                                                                                                                                                                                                                                                                                                                                                                    /note= "encoded by ACC"
                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
227
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                                        AAY05661 standard; Protein; 375 AA
                                                                                                                                                                                      Maize caffeic O-methyltransferase.
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97US-0057082.
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Best Local Similarity 37,33
Matches 139; Conservative
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N-PSDB; AAX25200.
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                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-AUG-1998;
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27-AUG-1997;
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                                                                                                                                      19-JUL-1999
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                                                                                                                                                                                                                                                                                    Zea mays.
                                                                                        AAY05661,
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                                                      191
                                                                                                                                                                                ADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVTELKLL 311
                                                                                                                 EGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a caffeic O-methyltransferase of maize, encoded by a clone (see AAX5201) isolated from a line A632 library. The invention provides methods and compositions relating to altering lignin biosynthesis and/or the lignin composition of plants. Isolated mucleic acids (see AAX5196-216) that code for plants. Isolated mucleic acids (see AAX5196-216) that code for colling (see AAX05657-77) involved in lignin biosynthesis are claimed. Also claimed are recombinant expression cassettes, host cells (especially maize or sorghum), and transgenic plants and seeds. The claimed nucleic acids can be used to transform a plant or modulate lignin biosynthesis. A claimed method involves transforming a plant cell with a recombinant expression cassette computating a lignin biosynthesis polymucleotide for a time sufficient a promoter, growing the plant cell under plant growing conditions, and inducing expression of the polymucleotide for a time sufficient computations can be used as a fuel source, material of increased lignin content can be used as a fuel source, and in the pulp and paper industry. Decreased lignin content
                                                  KRWVHEEDLIVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAF----RDCNWVF
                                                                         Maize; corn; caffeic O-methyltransferase; lignin; transgenic plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding plant lignin biosynthesis enzymes - used to transform plants to modulate lignin biosynthesis
                                                                                                                                                                                                                                             312 MDVHMACIINGKERKEEDWKKLFMEAGFQSYKISPFTGYLSLIEIYP 358
                                                                                                                                                                                                                                                                   Claim 9; Page 95-96; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maize caffeic O-methyltransferase
                                                                                                                                                                                                                                                                                                                                                              AAX05662 standard; Protein; 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bowen BA, Helentjaris TG,
                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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N-PSDB; AAX25201.
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27-AUG-1997;
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                                                                                                                                                                     --SSELSLAPWVEYFLEPNCQG-----AWNQLKR-------WVHEEDLT 145
                                                                                                                                                                                                                              118 EVSTATTLAPFVSLALQPIAASPHALGICAWFRQEQHEPSPYGLAFRQTPTLWEHADDV- 176
                                                                                                                                                                                                                                                       146 VFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQ-MINLAFRDCNWVFEGLESIVDVGGGT 204
                                                                                                                                                                                                                                                                                                                                 217 GGAAAAIAAAFPHVKCSVLDLPHVVAGAPSDGNVQFVAGNMFESIFPATAVFLKKTLHDN 276
                                                                                                                                                                                                                                                                                                                                                                        265 NDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVTELKLLMDVHMACIINGKE
                                                                                                   1 MASSLNNGRKASEIFQGQALLYKHLLGFIDSKCLKWMVELDIPDIIHSHSGQPITFSEL
                                                                                                                                                                                                                                                                                                        205 GITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVLLKLVLHNW
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maize; corn; caffeic O-methyltransferase; lignin; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding plant lignin biosynthesis enzymes – used to transform plants to modulate lignin biosynthesis
                                                                            62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a caffeic O-methyltransferase of maize,
                                                    Length 370;
                                                                            Indels
                                                                            132;
                                                   , DB 20;
1.7e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                          336 RDEQEWKKIFAEAGFKDYKILPVIGDVSVIIEVYP 370
                                                                                                                                                                                                                                                                                                                                                                                                          RKEEDWKKLFMEAGFQSYKISPFTGYLS-LIEIYP 358
improves the digestibility of fodder crops.
                                                                            64; Mismatches
                                                   30.1%; Score 567; 34.7%; Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Page 96-97; 166pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY05663 standard; Protein; 366 AA.
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97US-0057082
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                                                                           Conservative
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                                                              Local Similarity
les 137; Conserv
                          370 AA;
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99US-0137724.
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21-APR-1999;
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04-MAY-1999;
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18-MAY-1999;
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23-JUN-1999
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            11;
cancoded by a clone (see AAX25202) isolated from a maize line B73 cDNA library. The invention provides methods and compositions relating to altering lighin biosynthesis and/or the light composition of plants. Isolated nucleic and/or the light code for plants. Isolated nucleic acks (see AAX25196-216) that code for proteins (see AAV6567-77) involved in light biosynthesis are claimed. Also claimed are recombinant expression cassettes, host seeds. The claimed nucleic acks can be used to transform a plant cells (especially maize or sorghum), and transgenic plants and cransforming a plant cell with a recombinant expression cassette comprising a plant cell with a recombinant expression cassette comprising a plant cell with a recombinant expression of assette comprising a plant cell with a recombinant expression of and inducing expression of the polynucleotide operably linked to a promoter, growing the plant cell under plant growing conditions, and inducing expression of the polynucleotide for a time sufficient to modulate (preferably increase) light biosynthesis in the plant. The plant lightin content can be used as a fuel source, material of increased light content can be used as a fuel source, and in the pulp and paper industry. Decreased light content caps.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214
                                                                                                                                                                                                                                                                                                                                                                                TROVOSIMRYLAHNGFFEIVRIHDNIEA-----YALTAASELLVKSSE----LSLAPM 119
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                                                                                                                                                                                                                                                                                                                              11 ASEIFQGQALLYKHLLGFIDSKCLKWWVELDIPDIIHSHSHGQPITFSELVSILQVPPTK
                                                                                                                                                                                                                                                                                                                                               SOULLEAHDELFHHCLCFAKSLALAVAQDLRIPDAIHHHGGG--ATLHQILAEAALHPSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        275 NCKEAISGESKIGKVVVIDTVINBNKDERQVTELKLLMDVHMACIINGKERKEEDWKKLF
                                                                                                                                                                                                                                                                          28.7%; Score 540.5; DB 20; Length 366;
Llarity 33.3%; Pred. No. 1e-47;
Conservative 70; Mismatches 125; Indels 61;
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Best Local Similarity
Matches 128; Conserv
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4.5EP-1999; 99US-0155659. 4.5EP-1999; 99US-0155656. 4.5CT-1999; 99US-0155656. 5.5CT-1999; 99US-015717. 5.5CT-1999; 99US-015782. 8.5CT-1999; 99US-015802. 8.5CT-1999; 99US-015902. 8.5CT-1999; 99US-015902. 8.5CT-1999; 99US-01507. 8.5CT-1999; 99US-016076. 8.5CT-1999; 99US-016140. 8.5CT-1999; 99US-016140. 8.5CT-1999; 99US-016133. 8.5CT-1999; 99US-016133. 8.5CT-1999; 99US-016133. 8.5CT-1999; 99US-016132. 8.5CT-1999; 99US-016132. 8.5CT-1999; 99US-016132.	ry Match t Local Similarity 34.1%; Pred. No. 2.6e-46; ches 126; Conservative 70; Mismatches 151; Indels 22; Gaps 10;	6 NNGRKA-SEIFQGQALLYKHLLGFIDSKCLKWMVELDIPDIIHSHSHGQPITFSELVSIL 64 3 DNKRKVLDEBAKASLDIWKVVFGFADIAAAKCAIDLKIPEAIENHPSSQPVTLAELSSAV 62	65 QVPPTKTRQVQSLARXLAHNGFFEIVRIHDNI-EAYALTAASELLVKSSELSLAPRVE 121	122 YFLEPNCQGAMNQLKRWVHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDS 177 :	178 -QMLNLAFRDCNWVPEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSN 236 ::: : : : : : : : : : : : : : : : : :	237 NLTFVGGDMFKCIPKADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVI 296 :	297 NENKDERQVTELKLIAD-VHMACIINGKERKEEDWKKLFWEAGFQSYKISPFT 348	
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RESULT 12 AAG40136

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                                                 Arabidopsis thaliana protein fragment SEQ ID NO: 49760.
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                                                                                   termination sequence
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297 NENK-----DER--QVTELKLLMD-VHMACIINGKERKEEDWKKLFMEAGFQSYKISPFT 348
194 RRVVPRVAGACHGLFDGVTTMVDVGGGTGETMGMLVKEFPWIKGFNFDLPHVIEVAEVLD 253
                                                                                                         312 GENKKTMIVDERDEKLEHVRLMLDMYMMAHTSTGKERTLKEWDFVLKEAGFARYEVRDID 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 QVPPTKTRQVQSLMRYLAHNGFFEIVRIHDNI-EAYALTAASE--LLVKSSELSLAPMVE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                254 GVENVEGDMFDSIPACDAIFIKWVLHDWGDKDCIKILKNCKEAV--PPNIGKVLIVESVI
                               NLTFVGGDMFKCI PKADAVLLKLVLHNWNDNDCMKI LENCKEAI SGESKTGKVVVI DTVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; SEQ ID NO 2459; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.1%; Pred. No. 2.88-30,
ive 70; Mismatches 151; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.9%; Score 527; DB 23; 34.1%; Pred. No. 2.8e-46;
                                                                                                                                                                                                                                                                                                                                           Herbicidally active polypeptide SEQ ID NO 2459.
                                                                                                                                                                                                                                                                                                                                                                          Herbicidal; plant; agriculture; herbicide
                                                                                                                                                                                                                                                       ABB93248 standard; Protein; 382 AA.
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                    122 YFLEPNCQGAWNQLKRW----VHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDS 177
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                                                                                                                                                                                               254 GVENVEGDMFDSIPACDAIFIKWVLHDWGDKDCIKILKNCKEAV--PPNIGKVLIVESVI 311
                                                                                                                                                                                                                                                                          312 GENKKTMIVDERDEKLEHVRLMLDMVMMAHTSTGKERTLKEMDFVLKEAGFARYEVRDID 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein identification, signal transduction pathway, metabolic pathway, hybridisation assay, genetic mapping, gene expression control, promoter,
                                                                                          178 -OMINLAFRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 GVENVEGDMFDSIPACDAIFIKWVLHDWGDKDCIKILKRNCKEAV--PPNIGKVLIVESVI 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297 NENK-----DER--QVTELKLLMD-VHWACIINGKERKEEDWKKLFMEAGFQSYKISPFT 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 GENKKTMIVDERDEKLEHVRLMLDMVMAAHTSTGKERTLKEWDFVLKEAGFARYEVRDID 357
                                                                                                                                                                                                                                                                                                                                                                                                                                           65 QVPPTKTRQVQSLMRYLAHNGFFBIVRIHDNI-BAYALTAASE--LLVKSSELSLAPPMVE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 YFLEPNCQGAWNQLKRW----VHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDS 177
                                                                                                                                                                                                                                                                                                                                64
                                                                                                                                                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                 27.6%; Score 521; DB 21; Length 36 ilarity 33.9%; Pred. No. 1.1e-45; Conservative 70; Mismatches 152; Indels
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            990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
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US-08-91-677-6

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US-09-500-569-18

US-09-500-569-18

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59		10.0	621	m	US-09-059-522-1		1.1.4.4
3.0	189.5	10.0	621	m	-09-382-027	equence 1,	7 7
31			115	4	-09-266		4 4
32	135.5	7.2	368	4	-09-252-	equence 204	1777
33			139	4	US-09-252-991A-20476	equence 204	7 (2)
34	122.5	•	231	4	US-09-500-569-20	eduence 20	2
35	120.5	•	117	4	US-09-266-965-5	equence 5.	4
36	119		94		-08-266-451B	equence 20	A
37	119		94	N	-08-748-725-2	emience 20	4
38	110.5	5.0	115	4	-09-266-965-	egilence 4	A
<u>წ</u>	98.5		1890	4	-09-004-838-	ά	14
40	86	•	541	N	-08-540-804-1	equence 16	A
41	96		541	7	-218-265-1	emience 16	4 4
42	96		541	m	372	or entering	4
43	98	•	541	٣	99-1	emience 16.	Z Z
44	7.		983	Ŋ	US-08-449-645A-21	emience 21	. 4
45	97.5	•	983	(1)	-08-702-367A	equence 21,	Appl

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 M-ACDSQMLNLAFRDCNWVFEGLESIVDVGGGTGIT--AKIICEAFPKLKCMVLERPNVV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230 ENLSGSN-NLTFVGGDMFKCIPKADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237 ATKPADGAMINYVGGDMFSFIPPAQTVVLKLVLHHLTDEECVKLLAQCRKAIPSRKDGGK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVVIDTVINENKDERQVTELKLLMDVHMACIINGKERKEEDWKKLFMEAGFQSYKISPFT 348
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US-08-845-742-2

| Sequence 2, Application US/08845742C
| Patent No. 2573229
| GENERAL INFORMATION:
| APPLICANT: Walton, Jonathan D
| APPLICANT: Walton, Jonathan D
| TITLE OF INVENTION: Gene Encoding Herbicide Safener Binding Protein
| TITLE OF INVENTION: 69-000007
| CURRENT PAPLICATION NUMBER: US/08/845,742C
| UNMER OF SEQ ID NOS: 9
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 2
| LENGTH: 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 SEIFQGQALLYKHILGFIDSKCLKWMVELDIPDIIHSHSHGQPITFSELVSILQVPPTKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 ROVQSLMRYLAHNGFFEIVRIHDNIEAYALTAASELLV-----KSSELSLAPMVEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 22.6%; Score 426; DB 2; Length 363; Best Local Similarity 31.4%; Pred. No. 9.2e-36; Matches 116; Conservative 70; Mismatches 144; Indels
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                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Zea mays
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206 DVGGGTGATVAMIVSKYPSIKGINFDLPHVIGDAPTYPGVEHVGCDMFASVPRADAIFMK 265
                                                                                                  266 WICHDWSDEHCLKFLKNCYZBLPA---NGKVIIAECILPEAPDTSLATKNTVHVDIVMLA 322
                                                                       259 LVLHNWNDNDCWKILENCKBAISGESKIGKVVVIDTVINENKDERQVTELKLLMDVHM-A 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 LKWMVELDIPDIIHSHSHGQPITFSELVSILQVPPTKTR----QVQSLMRYLAHNGFFEI 89
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20.0%; Score 376.5; DB 2; Length 364;
Best Local Similarity 30.4%; Pred. No. 1.3e-30;
Matches 98; Conservative 69; Mismatches 136; Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APFLICANT: KNIGHT, www., Marc
APPLICANT: VAN MONTAGU, Marc
APPLICANT: LEGRAND, Michel
APFLICANT: LEGRAND, Michel
TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
                                                                                                                                                                     318 CIINGKERKEEDWKKLFMEAGFQSYKISPFTGYLSLIEI 356
                                                                                                                                                                                                            323 HNPGGKERTEKBFEALAKGAG------FTGFARLVAL 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
IR/O8/204,288
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CUSHMAN DARBY & CUSHMAN, L.L.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 10-MAR-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9119279.9
FILING DATE: 10-SEP-1991
PRIOR APPLICATION NUMBER: PCT/GB92/01460
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/204,288
FILING DATE: 10-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                   VAN DOORSSELAERE, Jan
FRITIG, Bernard J.M.
INZE, Dirk G.
JOUANIN, Lise
KNIGHT, Mary E.
VAN MONTAGU, Marc
                                                                                                                                                                                                                                                                                         RESULT 3
US-08-204-288-2
Sequence 2, Application US/08204288
; Patent No. 5959178
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TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: KOKULIS, Paul N. REGISTRATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington
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(: U.S.A.
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 LTV-----FEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVFEGLESIV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 IVRIHDNIEAYALTAASELLVKSSE-LSLAPWVEYFLEPNCQGAWNQ----LKRWVHEED 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 DVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVLLK 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 LKWMVELDIPDIIHSHSHGQPITFSELVSIL----QVPPTKTRQVQSLMRYLAHNGFFE 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 LKSAVELDLLELMAKAGPGAAISPSELAAQLSTQNPEAPVMLDRMLRLLASYSVLNCTLR 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.7%; Score 390.5; DB 2; Length 364; 30.4%; Pred. No. 4.4e-32; tive 64; Mismatches 135; Indels 37;
                                                                                                                                                                                                                                                                                                     APPLICANT: LEGRAND, Michel
TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
TITLE OF INVENTION: PLANTS
OVERESPONDENCE: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLII.
STATE: D. C.
COUNTRY: U.S.A.
COUNTRY: U.S.A.
COUNTRY: U.S.A.
ZIP: 20005-3518
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,288
TILING DATE: 10-MAR-1994
TILING DATE: 10-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION

APPLICATION

FILING DATE: 10-MAR-1994

CLASSIFCATION DATA:

APPLICATION NUMBER: 6B 9119279.9

FILING DATE: 10-SEP-1991

FILING DATE: 10-SEP-1991

FRIOR APPLICATION NUMBER: PCT/GB92/01460

APPLICATION NUMBER: PCT/GB92/01460

APPLICATION NUMBER: 16.773

APPLICATION NUMBER: 16.773

REFERENCE/DOCKET NUMBER: 206860/SEE36543/UST

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFAX: (202) 861.3000

TELEFAX: (202) 862-0944

TELEFAX: 6720 B02-0944

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 364 amino acids

"WDF: Amino acids

"WDF: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                              SEE: CUSHMAN DARBY & CUSHMAN, L.L.P.: 1100 New York Avenue, N.W.
Washington
                                                                                                                                                                       VAN DOORSSELAERE, Jan
FRITIG, Bernard J.M.
                                                                               US-08-204-288-5; Sequence 5, Application US/08204288; Patent No. 5959178; GRNERAL INFORMATION:
                                                                                                                                                                                                                    INZE, Dirk G.
JOUANIN, Lise
KNIGHT, Mary E.
VAN MONTAGU, Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 30.4
Matches 103; Conservative
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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-----BIVRIHDNIEAYALTAASELLVKSSE-LSLAPMVEYFLEPNCQGAWNQLKRW 138
                                                                                                               SLKDLPDGKVERL-----YGLAPVCKFLTKNEDGVSVSPLCLMNQDKVLMESWYYLKDA 146
                                                                                                                                                                                          205
                                                                                                                                                                                                                                                                                                             266 WICHDWSDAHCLKFLKNCYDAL---PENGKVILVECILPVAPDTSLATKGVVHVDVIMLA 322
                                                                                                                                                                                                                                                                                         259 LVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVTELKLLMDVHM-A 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 HNGFFEIVRIH------DNIEAYA-----LTAASELLVKSSELSLAPMVEYFLEPNC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 QGAWNQLKRWVHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCN 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 HGFDGISVLVDVGGGTGVTLKMIJSRYKHITGVNFDLPHVISQAPSLPGVNHVAGNMFES 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 IPKADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVTEL 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92
              87
       34 LKWWVELDIPDIIHSHSHGQPITFSELVSILQVPPTKTR----QVQSLMRYLAHNGFF--
                                139 VHEEDLIVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVFEGLESIV
                                                                                                                                                                                                                       DVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 S---FNVVRCSTEAGPGGDPLRRYSPAPVCRWFTAGD-----NHQGSLAPRLMLDVDEDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 WVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 GFIDSKCLKMMVELDIPDIIHSHSHGQPIIFSELVSILQVPPIKTRQ-----VQSLMRYLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jennie
TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs
FILE REFERENCE: Ball 27 US NA
CURRENT APPLICATION NUMBER: US/09/500,569
CURRENT FILING DATE: 2000-02-09
EARLIER APPLICATION NUMBER: 60/119,587
BARLIER FILING DATE: 1999-February-10
NUMBER OF SEQ ID NOS: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 29.7%; Pred. No. 1.3e-29;
Matches 104; Conservative 70; Mismatches 142; Indels
                                                                                                                                                                                                                                                                                                                                                              CIINGKERKEEDWKKLFMEAGFOSYKI 344
                                                                                                                                                                                                                                                                                                                                                                                    323 HNPGGKERTEKEFEGLAKGAGFQGFEV 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/09500569
Patent No. 6329204
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-500-569-16
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                                                                                                                                        TGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVLLKLVLHN 263
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8
VRIHDNIEA----YALTAASELLVKSSE-LSLAPMVEYFLEPNCOGAWNOLKRWVHEED 143
                                                                            203
                                                                                                                                                                                                            264 WNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVTELKLIMDVEM-ACIING 322
                                92 CSLKDHPDGKVERLYGLAPVCKFLTKNEDGVSVSPLCLMNQDKVLMESWYYLKDAILDGG 151
                                                                                                                                                                  LIVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVFEGLESIVDVGGG
                                                                                                      152 IP-PNKAYGMTAFEYHGTDPRFNKVFNKGMSDHSTITMKKILETYKGFBGLTSLVDVGGG
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MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage COMPUTER: IRM PC compatible OPERATING SYSTEM: MS DOS 6.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.7%; Score 371.5; DB 2; 29.7%; Pred. No. 4.2e-30; iive 69; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WordPerfect for Windows 5.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/715,325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Michael, Best & Friedrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 19,482
REFERENCE/DOCKET NUMBER: 66040/9627
TELECOMMUNICATION:
TELEPHONE: (414) 271-6560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: United States of America
                                                                                                                                                                                                                                                                                 323 KERKEEDWKKLFMEAGFOSYKI 344
                                                                                                                                                                                                                                                                                                       STREET: 100 E. Wisconsin Avenue CITY: Milwankee STATE: Yisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08715325
Patent No. 5886243
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Chiang, Vincent APPLICANT: Tsai, Chung-Jui APPLICANT: Podila, Gopi TITLE OF INVENTION: Genetic TITLE OF INVENTION: in Plan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Gemignani, Joseph A
REGISTRATION NUMBER: 19,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (414) 277-0656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    365 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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no
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CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches 97; Conserv
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TYPE: PRT
ORGANISM: Glycine max
FEATURE:
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Best Local Similarity
Matches 100; Conserv
                                                     ; NAME/KEY: UNSURE
; LOCATION: (134)
US-09-500-569-18
                                                                                                                  Query Match
Best Local S
Matches 99
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Patent No. 6329204
GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Shori, Jennie
TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs:
FILE REFERENCE: BB1327 US NA
CURRENT FILMG DATE: 2000-02-09
CURRENT FILMG DATE: 2000-02-09
EARLIER FILMG DATE: 1999-February-10
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 18
LENGTH: 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 LKWMVELDIPDIIHSHGPPITFSELVSILQVP---PTKTRQVQSLMRYLAHNGF--FE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEHCLKFLKNCYEAL---PDNGKVIVAECILPVAPDSSLATKGVVHIDVIMLAHNPRGKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                           US-09-500-569-4
Sequence 4, Application US/09500569
Fatent No. 6329204
GENERAL INFORMATION:
APPLICANN: Caboon, Rebecca E.
APPLICANN: Caboon, Rebecca E.
APPLICANN: Shen, Jennie
TITLE OF INVENTION: Plant Caffeic acid 3-0-Methyltransferase Homologs
TITLE OF INVENTION Plant Caffeic acid 3-0-Methyltransferase Homologs
FILE REPERENCE: BB1327 US NO.
CURRENT APPLICATION NUMBER: US/09/500,569
CURRENT FILING DATE: 2000-02-09
SEARLIER RPLING DATE: 1999-February-10
NUMBER OF SEQ ID NOS: 28
320 PLRMDVMMINNLRGGKIRTEQEYAKLAMDSGFSGSFRTTYIFANFMAIEL 369
                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                                                                                                                                                                                                                                              Score 364.5; DB 4; Length 365; Pred. No. 2.2e-29;
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Mismatches 138; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                             67;
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                                                                                                                                                                                                                                                                                                  SOFTWARE: Microsoft Office 97
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Best Local Similarity 31.23
Matches 100; Conservative
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; ORGANISM: Glycine max
US-09-500-569-4
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US-09-500-569-18
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                                                                                                                                                                                                                                                                                                           268 DCWKILENCKEAISGESKTGKVVVIDTVINENKDERQVTELKLLMDVHMACIINGKERKE 327
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                                                                                                                                                                                                                                                                                                                                                                                                 208 AKIICBAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVLLKLVLHNWNDN
                                                                                           34 LKWMVELDIPDIIHSHSHGQPITFSELVSILQV-PPIKTRQVQSLMRYLA-HNGFPEIVR
                                                                                                                                      36 LKSALELDLIEITAKAGPGVHLSPSDIASRLPTHNPDAPVMLDRILRLLACYNILSFSLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Chicatow, incent L
APPLICANT: Chicatoway, Daniel T
APPLICANT: Carraway, Daniel T
APPLICANT: Carraway, Daniel T
APPLICANT: Smelzer, Richard H
TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
FILE REFERENCE: 506.7
CURRENT PAPLICATION NUMBER: US 60/991,677A
CURRENT FILING DATE: 1997-12-16
EARLIER APPLICATION NUMBER: US 60/033,381
EARLIER PILING DATE: 1996-12-16
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 368;
         Length 358;
18.9%; Score 357; DB 4; Length 35 30.7%; Pred. No. 1.38-28; ive 65; Mismatches 140; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ED-----WKKLFMEAGFOSYKI 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 332 KRKSLRLWAK---GSGFQGFQV 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-991-677-6; Sequence 6, Application US/08991677A; Patent No. 6252135; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Liquidambar styraciflua
US-08-991-677-6
                       Similarity 30.7
99; Conservative
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76 SIMRYLAHNGFF--EIVRIHDN----IEAYALTAASELLVKSSE-LSLAPMVEYFLEPNC 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 QGAWNQLKRWVHEEDLTVFEVSLGTPF-----WDFINKDPAYNKSFNEAMACDSQM 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 LLSSSVLPFV----LHSTIQLEVPEIL-AKSNDTKLSASQIVS--QIPNCKNPDAATMLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 KDERQ----VTELKLLMDVHMACIINGKERKEEDWKKLFMEAGFQSYKI 344
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    APPLICANT: KNIGHT, Mary E.
APPLICANT: VAN MONTAGU, Marc
APPLICANT: LEGRAND, Michel
TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
TITLE OF INVENTION: PLANTS
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 131; Indels
                                                                                                                                                                                                                                                                    ZIP: 20005-3518
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.9%; Score 337; DB 2;
Similarity 27.5%; Pred. No. 1.6e-26;
06; Conservative 76; Mismatches 131.
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                                                                                                                                                                                1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,288
FILING DATE: 10-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: GB 9119279.9
FILING DATE: 10-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 206
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                       Washington
                                                                                                                                                                                                                             : D. C. RY: U.S.A. 20005-3518
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                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                  STREET:
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CNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMF 246
                                                                                 247 KCIPKADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVT 306
                                                                                                            94 DNIEA-----YALTAASELLVK-SSELSLAPMVEYFLEPNCOGAWNOLKRWVHEEDL 144
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APPLICANT: Cahoon, Rebecca E.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Shen, Jennie
TITLE OF INVENTION: Plant Caffeic acid 3-0-Methyltransferase Homologs
FILE REFERENCE: BB132 108 NA
CURRENT APPLICATION NUMBER: US/09/500,569
CURRENT FILING DATE: 2000-02-09
EARLIER FILING DATE: 1999-February-10
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 12
LENGTH: 354
                             196 TYKGFEGLGSVVDVGGGTGAHLNMITAKYPMIKGINFDLPHVIEEAPSYPGVEHVGGDMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 VELDIPDIIHSHSHGOPITFSELVSILQVPPTKTRQ----VQSLMRYLAHNGFFBIVRIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 TVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVFEGLESIVDVGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 IELGIFDIIAKAGEGAKLSAKDIAAKL---PCKNSEGATMLDRILKLLVCHSIIDCTVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 PFNRVH-GKHVFEYSDMNSSFNQLFMAAMTNRATLIMKKIVESYKGFEHINSLVDVGGGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 354;
                                                                                                                                                                     BLKLLMDVHM-ACIINGKERKEEDWKKLFMEAGFQSYKISPFTGY 350
                                                                                                                                                                                                  17.9%; Score 338.5; DB 4; Length 26.4%; Pred. No. 1.1e-26; Live 74; Mismatches 147; Indels
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                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/09500569 Patent No. 6329204
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Patent No. 5959178
GENERAL INFORMATION:
APPLICANT: VAN DOORSSELAERE, Jan
APPLICANT: RRITIG, Bernard J.M.
APPLICANT: INZE, Dirk G.
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) ORGANISM: Glycine max

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89; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                139 VHEEDLIV-----FEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVFBG 193
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                                      Sequence 14, Application US/09500569
Fatent No. 6329204
GENERAL INFORMATION.
FAPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jennie
TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs
FILE REFERENCE: BB1327 US NA
CURRENT FILING DATE: 2000-02-09
EARLIER APPLICATION NUMBER: US/09/500,569
CURRENT FILING DATE: 1999-February-10
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 LKWMVELDIPDIIHSHSHGQPITFSELVSILQVP----PTKTRQVQSLMRYLAHNGFFEI
                                                                                                                                                                                                                                                                                                                                                                     35 LKNAIELGMLEILVG-AGGKMLSPSEVAA--QLPSKANPEAPVMVDRMLRLLASN----
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                           45;
                                                                                                                                                                                                                                                                                                   Length 362;
                                                                                                                                                                                                                                                                                             17.5%; Score 329.5; DB 4; Length 28.0%; Pred. No. 9.4e-26; tive 71; Mismatches 126; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 356
TYPE: PRT
ORGANISM: Triticum aestivum
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Best Local Similarity
                 RESULT 11
US-09-500-569-14
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                                                                                                                                                                                                                                                                   137 RWVHEEDLTV----PEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVF
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APPLICANT: Cahoon, Rebecca E.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Shan, Jennie
TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs
FILE REPERENCE: BB137 US NA
CURRENT APPLICATION NUMBER: US/09/500,569
CURRENT APPLICATION NUMBER: 60/119,587
EARLIER APPLICATION NUMBER: 60/119,587
EARLIER PILLING DATE: 1999-February-10
NUMBER OF SEQ ID NOS: 28
                                                                                                                  53;
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       DB 4; Length 356;
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                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308 LKLLMDVHMACIINGKERKEEDWKKLFMEAGFQSYK 343
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SEQ ID NO 10
LENGTH: 378
                                            94; Conservative
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ORGANISM: Oryza sativa
                     Similarity
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Best Local Similarity
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US-09-500-569-10
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Query Match
Best Local S:
Matches 94
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261 DAIFWKWVLHDWSDEHCVKILNKCYESL---AKGGKIILVESLIPVIPEDNLESHMVFSL 317
                  --NENKDERQVTEL 308
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            DAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVI-
                                                                                                                 318 DCHTLVHNQ---GGKERSKEDFEALASKTGFSTVDV 350
                                                                                        309 KLLMDVHMACIINGKERKEEDWKKLFMEAGFQSYKI 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.0%; Score 283.5; DB 4; 28.0%; Pred. No. 4.8e-21; cive 50; Mismatches 142;
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US-09-615-192A-274
'Sequence 274, Application US/09615192A
'Patent No. 6410718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Eucalyptus grandis
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Best Local S:
Matches 79
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KLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVTELKLLMDVHMA 317
                  93 HDNIEAYALTAASELLVKSSE--LSLAPMVEYFLEPNCOGAWNOL------KRWVH 140
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                                                                                                                                                                                                                                                                             APPLICANT: Tarczynski, Mitchell C.
APPLICANT: Jansen, Richard G.
APPLICANT: Jensen, Richard G.
APPLICANT: Jensen, Richard G.
APPLICANT: Behnert, Hans J.
TITLE OF INVENTION: Transgenic Plants With Enhanced Mannitol
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Quaries & Erady
STREET: P.O. Box 2113, First Wisconsin Plaza
CITY: Madison
STATE: WI
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
16.1%; Score 303; DB 1; Length 365;
Best Local Similarity 26.5%; Pred. No. 5.4e-23;
Matches 89; Conservative 61; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Microsoft Word, Version #5.5
CURRENT APPLICATION DATA:
                                                                               318 CIIN---GKERKEEDWKKLFMEAGF 339
                                                                                                    334 MLSNSRGGKERTELEFAKLATDSGF 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 9221490026
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/871,416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/186,833 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                              RESULT 14
US-08-186-833-4
Sequence 4, Application US/08186833
Patent No. 5563234
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (608)251-5000
TELEFAX: (608) 251-9166
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Seay, Nicholas J. REGISTRATION NUMBER: 27386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-186-833-4
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GENERAL INCORMATION:
APPLICANT Bloksberg, Leonard N.
APPLICANT Bloksberg, Leonard N.
APPLICANT HAVMKRAIA 11Kka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content;
FILE REFERENCE: 11000.1003.04/09/615,192A
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT PILING DATE: 2000-07-12
PRIOR RIPLING DATE: 1997-11-21
PRIOR REPLICATION NUMBER: US 08/713,000
PRIOR PILING DATE: 1996-09-11
PRIOR PILING DATE: 1996-09-11
PRIOR PILING DATE: 1996-09-11
PRIOR PILING DATE: 1996-09-11
PRIOR FILING DATE: 1996-09-11
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al Similarity
139; Conserv
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Best Local S.
Matches 139
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Sequence 103, App
Sequence 102, App
Sequence 182, App
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Appli
Appli
Appli
                                                                                                      November 10, 2003, 03:21:21; Search time 76 Seconds (without alignments) 809.030 Million cell updates/sec
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Sequence 6,
Sequence 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5,
Sequence 6,
Sequence 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1
Sequence 1
Sequence 2
Sequence 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                     US-09-868-547-4
1886
1 MASSLNNGRKASEIFQGQAL......FQSYKISPFTGYLSLIEIYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published Applications AA:*

1: \cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

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17: \cgn2_6/ptodata/2/pubpaa/USO8_NBM PUB.pep:*

18: \cgn2_6/ptodata/2/pubpaa/USO8_NBM PUB.pep:*

18: \cgn2_6/ptodata/2/pubpaa/USO8_NBM PUB.pep:*
           GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-361-460-5

US-11-361-460-7

US-10-361-460-4

US-10-361-460-4

US-09-947-027-6

US-09-947-027-6

US-10-289-757-103

US-10-289-757-102

US-10-289-757-102

US-10-289-757-104

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                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                          - protein search, using sw model
                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match Length
                         Copyright
                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        540.5
435.5
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3371.5
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3371.5
331.5
323.5
323.5
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567
                                                                           OM protein
                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                      Searched:
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                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6449678890H2H4H
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16 273.5 14.5 351 15 US-10-267-255-133 Sequence 133, App 225.5 12.1 156 16 US-10-144-693-275 Sequence 275, App 19 225.5 12.0 331 15 US-10-156-761-10380 Sequence 10.30, App 225.5 12.0 331 15 US-10-156-761-10380 Sequence 15, App 22 190.5 10.7 145 16 US-10-156-761-919 Sequence 15, App 22 190.5 10.7 145 15 US-10-156-761-919 Sequence 270, App 22 190.5 10.7 145 15 US-10-156-761-919 Sequence 270, App 22 186.5 9.9 115 12 US-09-953-348-3 Sequence 3, Appl 22 166.5 9.9 115 12 US-09-953-348-5 Sequence 3, Appl 22 120.5 6.4 117 12 US-09-953-348-5 Sequence 3, Appl 22 120.5 6.4 117 12 US-09-953-348-5 Sequence 3, Appl 32 110.5 5.9 115 12 US-09-953-348-5 Sequence 3, Appl 33 15 US-10-267-255-4 Sequence 3, Appl 33 15 US-10-267-255-4 Sequence 3, Appl 34 97.5 5.9 115 12 US-09-953-348-5 Sequence 3, Appl 34 97.5 5.9 115 12 US-09-953-348-5 Sequence 3, Appl 34 97.5 5.2 983 12 US-10-166-75-9 Sequence 27, Appl 36 97.5 5.2 983 12 US-10-166-95-97 Sequence 27, Appl 36 97.5 5.2 983 12 US-10-166-95-97 Sequence 27, Appl 36 97.5 5.2 983 15 US-09-821-187-41 Sequence 27, Appl 37 96.5 5.1 952 11 US-09-821-187-41 Sequence 27, Appl 40 93.5 5.0 993 11 US-09-821-187-43 Sequence 42, Appl 40 93.5 5.0 993 11 US-09-821-187-43 Sequence 42, Appl 41 93.5 5.0 993 11 US-09-821-187-43 Sequence 30, Appl 44 93.5 5.0 993 11 US-09-821-187-43 Sequence 30, Appl 44 93.5 5.0 993 11 US-09-821-187-43 Sequence 30, Appl 44 93.5 5.0 993 11 US-09-821-187-43 Sequence 30, Appl 44 93.5 5.0 993 11 US-09-821-187-43 Sequence 30, Appl 44 93.5 5.0 993 11 US-09-821-187-43 Sequence 30, Appl 44 93.5 5.0 993 11 US-09-821-187-43 Sequence 30, Appl 44 93.5 5.0 993 11 US-09-881-881-881 Sequence 30, Appl 560.5 5.0 993 11 US-09-8
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ALIGNMENTS

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RESULT 1

US-10-5

US-10-5

US-10-5

Publication No. US20030163839A1

GENERAL INPORMATION:

APPLICANT: Helenipanin A.

APPLICANT: Helenipanin A.

APPLICANT: Bonen, Benjamin A.

APPLICANT: Wang Xun

TITLE OF INVENTION: Genes Encoding Enzymes for Lignin

TITLE OF INVENTION: Biosynthesis and Uses Thereof

CURRENT APLICATION WURBER: US/10/361,460

CURRENT PLING DATE: 1200-20-10

CURRENT APLICATION WURBER: 60/057,082

MUMBER OF SQ ID NOS: 85

CURRENT SPILING DATE: 1399-08-27

NUMBER OF SQ ID NOS: 85

CURRENT FILING DATE: 1399-08-27

NUMBER OF SQ ID NOS: 85

CORGANISM: Zea mays

US-10-361-460-5

MATCH: 37

MATCH: 37

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MATCH: 37

MATCH: MATCH: MATCHING MAT
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US-10-361-460-7
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 168 SFNEAMACDSQ-MLNLAFRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERP 226
                 NVVENLSGSNNLTFVGGDMFKCIPKADAVLLKLVLHNWNDNDCMKILENCKEAISGESKT 286
                                                                       GKVVVIDTVINENKDERQVTELKLLMDVHMACIINGKERKEEDWKKLFMEAGFQSYKISP 346
                                                                                                                               61 VSILQVPPTKTRQVQSLMRYLAHNGFFEIVRIH-----DNIEA---YALTAASELLVK- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 --SSELSLAPMVEYFLEPNCQG-----AWNOLKR--------WVHEEDLT 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.1%; Score 567; DB 12; Length 370; 34.7%; Pred. No. 1.8e-49; iive 64; Mismatches 132; Indels 62;
                                                                                                                                                                                                                                         US-10-361-460-6

Sequence 6, Application US/10361460

Sequence 6, Application US/10361460

Publication No. US20030163839A1

GENERAL INPORMATION:
APPLICANT: Helentjaris, Timothy G.
APPLICANT: Bowen, Benjamin A.
APPLICANT: Wang, Xun
ITLE OF INVENTION: Genes Encoding Enzymes for Lignin
ITLE OF INVENTION: Biosynthesis and Uses Thereof
FILE REFERENCE: 0709
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: 06/057,082
PRIOR PILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 85

SOFTWARE: PastSEQ for Windows Version 3.0

FEMALE OF TOWNEY OF SEC ID NOS: 85
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                                                                                                                                                                    347 FTGYLS-LIEIYP 358
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 FPHVKCSVLDLPHVVAGAPSDACVQFVAGNMFHSIPPATAVFFKTTLCDWGDDECIKILK 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 VEYFL-----EPNCOG--AWNQLKR--------WVHEEDLTVFEVSLGTPFW 156
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| SANLALHPIAISPHAVGICAWFRQEQHDPSPYGLAFRQIPTIWEHADNV-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215 FPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVLLKLVLHNWNDNDCMKILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          275 NCKEAISGESKTGKVVVIDTVINENKDERQVTELKLIMDVHMACIINGKERKEEDWKKLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 ASEIFQGQALLYKHLLGFIDSKCLKWMVELDIFDIIHSHSHGQPITFSELVSILQVPPTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 366,
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APPLICANT: Bowen, Benjamin A.
APPLICANT: Bowen, Benjamin A.
APPLICANT: Wang, Xun
TITLE OF INVENTION: Benes Encoding Enzymes for Lignin
TITLE OF INVENTION: Biosynthesis and Uses Thereof
FILE REPREBENCE: 0709
CURRENT APPLICATION NUMBER: US/10/361,460
CURRENT PILING DATE: 2003-02-10
FRICA APPLICATION NUMBER: 60/057,082
FRICA REPLING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28.7%; Score 540.5; DB 12; 33.3%; Pred. No. 9.5e-47; ive 70; Mismatches 125;
                                                                             APPLICANT: Helentjaris, Timothy G.
APPLICANT: Bowen, Benjamin A.
APPLICANT: Bowen, Benjamin A.
APPLICANT: Bowen, Benjamin A.
TITLE OF INVENTION: Genes Encoding Enzymes for TITLE OF INVENTION: BioSynthesis and Uses The FILE REFERENCE: 0709
CURRENT APPLICATION NUMBER: US/10/361,460
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: 60/057,082
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 85
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      343 IEAGFKDYKIRPVAGLMSVIEVYP 366
Sequence 7, Application US/10361460
Publication No. US20030163839A1
GENERAL INFORMATION:
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Publication No. US20030163839A1
GENERAL INFORMATION:
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Matches 128, Conservative
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ORGANISM: Zea mays
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WESULI 6
US-10-091-009-6
Sequence 6, Application US/10091009
Sequence 6, Application No. US20020138870A1
Sequence 6, Application No. US20020138870A1
GENERAL INFORMATION:
APPLICANT: Chiang, Vincent Lee C.
APPLICANT: Li, Langeng
TITLE OF INVENTION: METHODS FOR SIMULTANEOUS CONTROL OF LIGNIN CONTENT AND
TITLE OF INVENTION: COMPOSITION, AND
TITLE OF INVENTION: COMPOSITION, AND
FILLE REPERENCE: 066040-9718
CURRENT PILING DATE: 2002-09-06
FRIOR APPLICATION NUMBER: 09/947,027
PRIOR FILING DATE: 2000-09-05
PRIOR FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 6
FEMALY. 2000-09-05
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SEQ ID NO 6
FEMALY. 2000-09-05

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                                          139 VHEEDLIVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVFEGLESIV 198
                                                                                                                                                                                                                                                                         259 LVLHNWNDNDCMKILBNCKEAISGESKTGKVVVIDTVINENKDERQVTELKLLMDVHM-A 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 -----EIVRIHDNIEAYALTAASELLVKSSE-LSLAPMVEYFLEPNCQGAMNQLKRW 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139 VHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSOMLNLAFRDCNWVFEGLESIV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258
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                                                                               33 SLKDLPDGKVERL-----YGLAPVCKFLTROREDGVSVSPLCLMNQDKVLMESWYYLKDA
                                                                                                                                                           DVGGGTGTTAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVLLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 LKWMVELDIPDIIHSHSHGQPITFSELVSILQVPPTKTR-
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                                                                                                                                                                                                                                                                                                                                                                                             318 CIINGKERKEEDWKKLFMEAGFQSYKI 344
                                                                                                                                                                                                                                                                                                                                                                                                                                  323 HNPGGKERTEKEFEGLAKGAGFOGFEV 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: aspen populus tremuloides
US-10-091-009-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 29.7
Matches 97; Conservative
                                                                                                                                                           199
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APPLICANT: Chiang, Vincent Lee C.
APPLICANT: Li, Laigeng
TITLE OF INVENTION: METHODS FOR SIMULTANEOUS CONTROL OF LIGNIN CONTENT AND COMPOSITIC
TITLE OF INVENTION: CELLULOSE CONTENT IN PLANTS
FILE REFERENCE: 066040-9718
CURRENT APPLICATION WUMBER: uS/09/947,027
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: 60/230,086
PRIOR FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 PFLGRVWRLLVTSGVF---ASSDDVQ-YRLNPLSWLLVEGVESEDHTYQKYFVLGTVSRH 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 CQGAMNQLKRWVHEED-----LTVFEVSLGTPFWDFINK--DPAYNKSFNEAMAC-DSQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 YVEAGMSLADWFKKEEDEDRQLPSPFBALHGVPLVHESTKLLDBELDRVVEEGVAAHDN1 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 TIT------IPPAQAVMLKLVLHFWSDDDCVKILBLCRKAIPSRQEGGKVIIIEILL 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297 NENKDERQVTELKLIMDVHMACIINGKERKEEDWKKLFMEAGFOSYKISPFTGYLSLIEI 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 GPYMGP-VMYBAQLLMDWLMMVNTKGRQRGEDDWRHIFTKAGFSDYKVVKKIGARGVIEV 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------EIVRIHDNIEAYALTAASELLVKSSE-LSLAPMVEYFLEPNCQGAMNQLKRW 138
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                                                                                                                                                                                                                                                                                                                                                               10 AELLQAQADLWRHSLYYLTSMALKCAVELHIPTAI--HNLGGSATLPDLVAALSLPAAKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 MLNLAFRDCNW-VFEGLESIVDVGGGTG-ITAKIICEAFPKLKCMVLERPNVVENLSGSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 SEIFQGQALLYKHLLGFIDSKCLKWMVELDIPDIIHSHSGQPITFSELVSILQVPPTKT
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                                                                                                                                                                                                                                                                            32;
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                                                                                                                                                                                                               DB 12; Length 354;
                                                                                                                                                                                                                                                                         Mismatches 147;
                                                                                                                                                                                                            23.1%; Score 435; DB 1 34.0%; Pred. No. 6e-36;
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 4 LENGTH: 354 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: aspen populus tremuloides US-09-947-027-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 6, Application US/09947027
Patent No. US20020124281A1
GENERAL INFORMATION:
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Matches 97; Conserv
                                                                                                                                                                                                                                           Similarity
                                                                                                                       ; ORGANISM: Zea mays
US-10-361-460-4
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 -----SYSVLICŚLRILPDGKIERLYGĽÁPVCK-FĽIRNDDĠVSIAALSLMNQDKVL 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 TYKGFEGLGSVVDVGGGTGAHLNMILAKYPMIKGINFDLPHVIEEAPSYPGVEHVGGDMF
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Sequence 6, Application US/09796256A
Patent No. US20020078477A1
| Patent No. US20020078477A1
| APPLICANT: Chiang, Vincent L
| APPLICANT: Carraway, Daniel T
| APPLICANT: Carraway, Daniel T
| APPLICANT: Smeltzer, Richard H
| TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
| FILE REPERENCE: 5061/c-3532.0
| CURRENT APPLICATION NUMBER: US/09/796,256A
| CURRENT FILING DATE: 2001-02-28
| PRIOR APPLICATION NUMBER: US60/033381
| PRIOR FILING DATE: 1996-12-16
| PRIOR PILING DATE: 1997-12-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.6%; Score 350.5; DB 9; Length 368; 29.0%; Pred. No. 3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   307 ELKLLMDVHM-ACIINGKERKEEDWKKLFMEAGFQSYKISPFTGY 350
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APPLICANT: FORSTEY, Richard L
APPLICANT: Shenk, Michael Andrew
APPLICANT: Shenk, Michael Andrew
APPLICANT: Shenk, Michael Andrew
APPLICANT: Glenn, Matthew
APPLICANT: Glenn, Matthew
APPLICANT: Saulsbury, Kaith Martin
APPLICANT: Hall, Claire
TITLE OF INVENTION: Compositions isolated from forage
TITLE OF INVENTION: Grasses and methods for their use
FILE REFERENCE: 11000.1061U
CURRENT FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: 60/337,703
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 103, Application US/10289757
Publication No. US20030180751A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Liquidambar styraciflua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62;
                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
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Best Local
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196 EGLGSLVDVGGGVGATVAAIAAHYPTIKGVNFDLPHVISEAPQFPGVTHVGGDMFKEVPS 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 RWVHBEDLIV----FEVSLGTPFWDFINKDPAYNKSFNBAMACDSQMLNLAFRDCNWVF 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 ADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVI----NENKDERQVTE 307
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                                                                                                                                                                                                                                                                                                                                                                        EGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPK
                                                                                                                                                                                                                                                 34 LKWMVELDIPDIIHSHSHGQPITFSELVSIL--QVPPTKTRQVOSLMRYLAHNGFFELVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 SWYYLKDAVLDGGIPPNKAYGMSAFEYHGTDPRFNRVFNEGMKNHSIIITKKLLELYHGF
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                                                                                                                                                                                                                                                                              49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.9%; Score 337.5; DB 12; Length 28.6%; Pred. No. 6.3e-26; Live 62; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Demmer, Jeroen
APPLICANT: Porster, Richard L
APPLICANT: Glbson, John Bryan
APPLICANT: Glbson, Machael Andrew
APPLICANT: Glenn, Mathew
APPLICANT: Glenn, Greise and methods for their use
ITILE OF INVENTION: Compositions isolated from forage
ITILE OF INVENTION: Grasses and methods for their use
FILE REPERENCE: 11000.1061U
CURRENT APPLICATION NUMBER: G0/337,703
FRICR APPLICATION NUMBER: 60/337,703
FRICR APPLICATION NUMBER: 60/337,703
FRICR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 218
SOFTWARE: FastSEQ for Windows Version 4.0
IENNGTH: 360
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 102, Application US/10289757
Publication No. US20030180751A1
GENERAL INFORMATION:
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                                                                                                                                                                                                       96; Conservative
                                     ENGTH: 360
TYPE: PRT
CRGANISM: FLolium perenne
US-10-289-757-103
                                                                                                                                                                               Similarity
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Best Local Similarity
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                  SEQ ID NO 103
                                                                                                                                                       Query Match
Best Local S:
Matches 96
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ORGANISM: 1
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63 ILQVP---PTKTRQVQSLMRYLAHNGFFEIVRIHDNIEAYALTAASELLVK-----SS 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 RYGAAPVCK-FLTPNEDGVSMAALALMNQDKVLMESWYYLKDAVLDGGIPFNKAYGMSAF 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217 KLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVLLKLVLHNWNDNDCMKILENC 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 277 KEAISGESKTGKVVVIDTVINENKDERQ----VTELKLLMDVHMACIINGKERKEEDWKK 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GSTAAEIAASADEBACLYALQLGSSSILPWTLKNTIELGLLETLMA-AGGKSLTPTEVAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 GRKASEIFQG---QALLYKHLLG--FIDSKCLKWMVELDIPDIIHSHSHGQPITFSELVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 17.5%; Score 329.5; DB 12; Length Best Local Similarity 27.8%; Pred. No. 4.2e-25; Matches 103; Conservative 70; Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Content of the state        313 VDMIMLAHNP---GGRERYERFEALARGAGFTGVK 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/337,703
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 218
SOFTWARE: FASEEG OF Windows Version 4.0
                                                                                                                                                                                                                                   Sequence 105, Application US/10289757
Publication No. US20030180751A1
GENERAL INFORMATION:
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; Publication No. US20030180751A1
; GENERAL INFORMATION:
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APPLICANT: Forster, Richard L
APPLICANT: Gibson, John Bryan
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                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Demmer, Jeroen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CRGANISM: Lolium perenne
US-10-289-757-105
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GDAILMKWILHDWSDQHCATLLKNCYDALPAH---GKVVLVECILPVNPEAKPSSQGVFH 312
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252 ADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQ----VTB 307
                                                                                                                                                                                                                                                              192 EGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWYYLKDAVLDGGIPFNKAYGMSAFBYHGTDPRFNRVFNEGMKNHSIIITKKLLELYHGF 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92 IHDNIEAYALTAASELLVKSSELS----LAPMVEYFLEPNCQGA------WNQ----LK 136
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28.0%; Pred. No. 2.6e-25;
Live 65; Mismatches 128; Indels 49;
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APPLICANT: Glenn, Matthew
APPLICANT: Saulsbury, Keith Martin
APPLICANT: Hall, Claire
IIILE OF INVENTION: Compositions isolated from forage
TITLE OF INVENTION: grasses and methods for their use
FILE REFERENCE: 11000.1061U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          313 VDMIMLAHNP---GGRERYERFEALARGAGFIGVK 345
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CURRENT FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: 60/337,703
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 218
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 182, Application US/10289757
Publication No. US20030180751A1
GENERAL INFORMATION:
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APPLICANT: Gibson, John Bryan
APPLICANT: Shenk, Michael Andrew
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US-10-289-757-182
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Best Local Similarity 28.0%
Matches 94; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADAVILKLVIHNWNDNDCMKILENCKBAISGESKTGKVVVIDTVINENKDERQ----VTE 307
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                                                                                                                                                                                                                                                                                                                                                              Length 360;
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                                                                                                                                                                                                                                                                                                                                                       17.4%; Score 328.5; DB 12; Length 27.7%; Pred. No. 5.2e-25; ive 67; Mismatches 127; Indels
                                              APPLICANT: Saulsbury, Keith Martin
APPLICANT: Hall, Claire
TITLE OF INVENTION: Compositions isolated from forage
TITLE OF INVENTION: Grasses and methods for their use
FILE REPERENCE: 11000.1061U
CURRENT APPLICATION NUMBER: US/10/289,757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Rathinasabapathi, Bala
APPLICANT: Rathinasabapathi, Bala
APPLICANT: Raman, Suresh Babu
TITLE OF INVENTION: BETA-ALANINE N-METHYLITRANSFERASE
FILE REPERENCE: 5883-205-1CIP
CURRENT APPLICATION NUMBER: US/10/213,473
CURRENT FILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.5%; Score 293; DB 15; 25.6%; Pred. No. 2.4e-21; tive 69; Mismatches 154;
                    Geoffrey
                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/337,703
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 218
SOFTWARE: FastSEQ for Windows Version 4.0
              No. US20030180751Alriss,
Glenn, Matthew
Saulsbury, Keith Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 29, Application US/10213473 Publication No. US20030104598A1 GENERAL INFORMATION:
Shenk, Michael Andrew
                                                                                                                                                                                                                                                                                                 ORGANISM: Festuca arundinacea
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                                                                                                                                                                                                                                                                                                                                                                                            93; Conservative
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Best Local Similarity
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LENGIH: 37
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Best Local (
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Matches
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37 MVELDIPDIIHSHSHGQPITFSELVSILQVPP--TKTRQVQSLMRYLAHNGFFEIVRIHD 94

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95 NIEA-------YALTAASELLVKSSELSLAPMVEYFLEPNCQ----GAWNQLKRWV 139
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97 HLDTTSSSSSTSERRYCLTEVGQTLVSFDB-SCPSHGAYVLQHYGETLLKAMPPLHTAI 155
                                                                                                                                                                                  156 LDASTEPFARVNGEPAYQYYGKNDELNKUMQYAMSGVSVPYMKALLGSGYDGFEGVKTLV 215
                                                                                                                                                                                                                                        DVGGGTGITAKIICEAFPKL-KCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVLL 257
                                                                                                                                                                                                                                                                                                                         KLVLANWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVTELKLLMDVHMA 317
                                                                                                                                                                                                                                                                                                                                                             276 KWVLTCFTDEEVITLMRNCNKAL---PVGGKLICSEPTLPENSDESHRTRALLVADIFIM 332
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140 HEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNW-VFEGLESIV
                                                                                                                                                                                                                                                                                216 DVGGSSGDCLRMIINKYKDIPKAINFDLPEVVAKAPKIPGITHVGGNMFESVPSGDAIFV
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APPLICANT: Bloksberg, Leonard N.

APPLICANT: Bloksberg, Leonard N.

APPLICANT: Bloksberg, Leonard N.

TITLE OF INVENTION: Materials and Methods for the

TITLE OF INVENTION: Modification of Plant Lignin Content

FILE REFERENCE: 11000.1003c5

CURRENT APPLICATION NUMBER: US,10/174,693

CURRENT FILING DATE: 2002-06-18

PRIOR APPLICATION NUMBER: US 08/975,316

PRIOR APPLICATION NUMBER: US 08/713,000

PRIOR PILING DATE: 1996-09-11

PRIOR PILING DATE: 1998-10-09

PRIOR FILING DATE: 1998-10-09

PRIOR FILING DATE: 1998-10-09

PRIOR FILING DATE: 1098-10-09

PRIOR FILING DATE: 2000-07-12

NUMBER OF SEQ ID NOS: 407

SEQ ID NOS: 407
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                                                                                                                                                                                                                                                                                                                                                                                                            318 CI--INGKERKEEDWKKLFMEAGFQSYKISPFTGYLSLIE 355
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.0%; Score 283.5; DB 16; 28.0%; Pred. No. 1.9e-20; cive 50; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 274, Application US/10174693
Publication No. US20030131373A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Eucalyptus grandis
US-10-174-693-274
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Best Local Similarity
Matches 79; Conserv
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US-10-174-693-274
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85 GFFEIVRIHDNIEAYALTAASELLVKSSELSLAPMVEYFLEPNCQGAWNQLKRWVHEEDL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 TVFEV-----SLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWV-----FEG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 SFPSTWPTAPRSGSSP-----TRDPKARELFNRAMG-----SVSLTEAGOVAAAYDFSG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 LESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVEN----LSG---SNNLTFVGGDMF 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 KCIPK-ADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQV 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 LLGFIDSKCLKWWVELDIPDIIHSHSHGQPITFSELVSILQVPPTKTRQVQSLMRYLAHN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 14.5%; Score 273.5; DB 12; Length 351; Best Local Similarity 27.0%; Pred. No. 2.2e-19; Matches 95; Conservative 68; Mismatches 140; Indels 49;
                                                                                                           OS-095953-48-133
) Sequence 133, Application US/09953348
) Publication No US20030134398A1
) GENERAL INPORMATION:
APPLICANT: Sheaman, David. H
APPLICANT: Mao, Vingqing
APPLICANT: Waroglu, Mustafa
APPLICANT: Waroglu, Mustafa
APPLICANT: Beldon, Paul
TILLE OF INVENTION: MITOMYCIN BIOSYNTHETIC GENE CLUSTER
FILE REPERENCE: 600.5301831
CURRENT APPLICATION NUMBER: US/09/953,348
CURRENT APPLICATION NUMBER: PCT/US00/06394
PRIOR PILING DATE: 2000-03-10
PRIOR FILING DATE: 2000-03-10
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 153
SOFTWARE: FastsEQ for Windows Version 4.0
| SEQ ID NO 133
completed: November 10, 2003, 03:30:38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT; ORGANISM: Streptomyces lavendulae US-09-953-348-133
                                                                                                  US-09-953-348-133
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Job time : 7
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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 10, 2003, 03:09:40 ; Search time 43 Seconds (without alignments) 800.660 Million cell updates/sec Run on:

US-09-868-547-4 1886 1 MASSLNNGRKASELFQGQAL.......FQSYKISPFTGYLSLIEIYP 358 Title: Perfect score: Sequence:

Scoring table:

283308 segs, 96168682 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

pIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

rij	isoflavone-7-0-met	soflavone-0-meth	-methyltransfer	6a-hydroxymaackiai	catechol 0-methylt	ransfera	catechol O-methvlt	echo1	atechol	Safener	O-me	O-methyl	soliquiritigenin	-diphen	caffeate O-methylt	iqnin-b	probable caffeate	catechol O-methylt		hypothetical prote	0		-COA	100	Pin F91,11	Egic acid	o-inositol O-med	otherical n	hetical prot
SUI	925	70	29	œ	S52015	26	50	96	96	35	0	0	5	T12259	57	9	78	4	44	55	5	8	26	7	645	4616	69	9665	9680
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esult No.		2	m	4	Ŋ	w	_	ω	o,	10	11	12	13	14	15	16	17	18	61	50	23	22	23	24	25	26	27	28	53

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hypothetical prote	hypothetical prote		hypothetical prote	probable O-merhvlt	carminomycin 4-0-m	probable 0-methylt	O-demethylpuromyci	hypothetical prote	polyketide synthas	temN protein - Str	hypothetical prote	acetvlserotonin O-	acetvlserotonin O-	acetylserotonin O-	
G96804	B86344	E86344	C86344	D86344	A47128	F83120	JO1393	E96653	JC5855	S27696	F70932	A42106	\$21265	137463	T50751
N	~	(7)	7	~	7	~	~	~	N	N	N	~	N	~	~
381	373	373	373	373	356	334	376	205	341	494	339	345	346	373	379
15.0	14.8	14.8	14.4	14.4	14.2	13.6	13.4	13.0	12.8	10.7	10.6	10.3	10.2	6.9	0.6
283.5	278.5	278.5	272:5	271.5	268	257	252	245.5	240.5	202	200.5	194	192	176	170.5

ALIGNMENTS

1 1 4 4 8 8 1 1 1 6 1 1 1 1 6 1 1 1 1 6 1 1 1 1	RESULT 1 T09254 isoflavone-7-O-methyltransferase (EC 2.1.1) 9 - alfalfa isoflavone-7-O-methyltransferase (EC 2.1.1) 9 - alfalfa c;Species: Medicago sativa (alfalfa) C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000 C;Accession: T09254 R;He, X.2.; Reddy, J.T.; Dixon, R.A. Blant Mol. Biol. 36, 43-4, 1998 A;Hitle: Stress responses in alfalfa (Medicago sativa L.) XXII. cDNA cloning and A;Reference number: Z16628; MUID:98145455; PMID:948461	A; Accession: 199254 A; Accession: 199254 A; Molecule type: mRNA A; Residues: 1-352 cHBX> A; Residues: 1-352 cHBX> A; C; Genetics: C; Genetics: T. 10MT (9) C; Punction: catalyzes the 0-methylation of A-ring hydroxyl group(s) of isoflavones A; Note catalyzes the 0-methylation of A-ring hydroxyl group(s) of isoflavones C; Sunction: dictor-inductible	Ouery March Ger Local Similarity 68.2%; Score 1295; DB 2; Length 352; Marches 244; Conservative 55; Mismarches 53; Indels 6; Gaps 4;	1 MASSLANGRKASEIFQGQALLYKHLLGFIDSKCLKWMVELDIPDIIHSHSHGQPITFSEL 60	1 VSILQVPPTKTRQVQSIMRYLAHNGFFEIVRIHDNIEAYALTAASELLVKSSELSLAFMV 120	1 BYFLEPNCQGAWNQLKRWVHEEDLTVFBVSLGTPFWDFINKDPAYNKSFNBAMACDSQML 180	1 NLAFRDCHWVFBGLESIVDVGGGTGTTAKIICEAFPKLKCMYLERPNVVENLSGSNNLTF 240	1 VGGDMFKCIPKADAVILKLVIANWNDNDCMKILENCKEAISGESKTGKVVVDTVINENK 300
RESULT 1 T09254 isoflavone-7-O-methyltransfer C;Species: Medicago sativa (a C;Species: Medicago sativa (a C;Species: Medicago sativa (a C;Accession: T09254 R;He XZ.; Reddy, J.T.; Dixo Plant Mol. Biol. 36, 43-54, 1 A;Ttle: Stress responses in A;Accession: T09254 A;Status: preliminary; transl A;Becule type: mRNA A;Residues: 1-352 cHEXA A;Residues: 1-354 CONSERVASEIF C;Superfamily: O-methyltransferase C;Su	SULT 1 19254 Offlavone-7 Species: M Date: 11-J Accession: He, X.Z.; Ant Mol. B Title: S.E Reference	Accession: Status: pr Molecules: tr Residues: tr Residues	Query Matcl Best Local Matches 2					

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A, Description: methyltransferase
C, Superfamily: O-methyltransferase
C, Keywords: methyltransferase
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                                                                    Query Match
Best Local Similarity 66.5
Matches 238; Conservative
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Matches 174; Conservative
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                    Cipecies: Medicago sativa (alfalfa)
Cipaces: Medicago sativa (alfalfa)
Cipaces: Medicago sativa (alfalfa)
Cipace: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Nov-2000
Cipace: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Nov-2000
Cipace: 10-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Nov-2000
Cipacession: T0970, T02500.
A;Reference number: Z16628; MUID:98145455; PMID:9484461
A;Reference number: Z16628; MUID:98145455; PMID:9484461
A;Reference number: Z16628; MUID:98145455; PMID:9484461
A;Residues: T09707
A;Residues: 1-352 cHEX.
A;Residues: 1-352 cHEX.
A;Residues: 1-352 cHEX.
A;Residues: T09250
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-292, FE;294-352 cHE2.
A;Residues: 1-292, FE;294-352 cHE2.
A;Residues: 1-292, FE;294-352 cHE2.
C;Genetics:
                                                                                                                  CDNA cloning and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       o-methyltransferase (EC 2.1.1.-) iomt2003 - alfalfa
C;Species: Medicago sativa (alfalfa)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 26-Aug-1999
C;Accession: T02029
R;He, X.Z.; Dixon, R.A.
submitted to the EMBL Data Library, September 1997
A;Reference number: 216642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EYFLEPNCQGAWNQLKRWVHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQML
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A)Molecule type: mRNA
A)Residues: 1-343 <HEX>
A)Cross-references: EMBL:AF023481; NID:g2565272; PID:g2565273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.1%; Score 1285; DB 2;
67.6%; Pred. No. 1.7e-95;
live 57; Mismatches 53;
            isoflavone-O-methytransferase (EC 2.1.1.-) - alfalfa
                                                                                                                                                                                                                                                                                                                                                          C.Function:
A.Pescription: methyltransferase
A.Note: elicitor-inducible
C.Superfamily: O-methyltransferase
C.Keywords: methyltransferase
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nes 242; Conservative
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A) Description: catalyzes the methylation of (+)6a-hydroxymaackiain to (+)pisatin A;Pathway: the terminal step in the pisatin biosynthesis C;Superfamily: O-methyltransferase
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                                                                                                                                VSILQVPPTKTRQVQSLMRYLAHNGFFEIVRIHDNIBAYALTAASELLVKSSELSLAPMV 120
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                                                                                                                                                                                               EYFLEPNCQGAWNQLKRWVHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQML 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 HPSKVNILYRFLKLLTHNGFFAKTTVKSNEGEEETAYVLTPSSKLLVSGKSTCLSSLVKG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99
                                                                                                                                                                                                                                                                                                                                                                                                 DERQVIELKLIMDVHMACIINGKERKEEDDWKKLFMEAGFQSYKISPFTGYLSLIEIYP 358
                                                                                                                                                                                                                                                                                                                                                                                                                     236 VGGDMFTSIPNADAVLLK------DCLRILKKCKEAVTNDGKRGKVTIIDMVIDEKK
                                                                                                                                                        58 VSILQVPSSKIGNVRRIMRYLAHNGFFEIITKEE--ESYALTVASELLVRGSDLCLAPMV
                                                                                                                                                                                                                  181 NLAFRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTF
                                                           1 MASSLNNGRKASEIFQGQALLYKHLLGFIDSKCLKWWVELDIPDIHSHSHGQPITFSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 FLEPNCQGAWNQLKRWVHEE-DLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 NGRKASEIFQGQALLYKHLLGFIDSKCLKWMVBLDIPDIIHSHSHGQPITFSELVSILQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 PPTKTRQVQSLMRYLAHNGFFEIVRIHDN----IEAYALTAASELLVKSSELSLAPMVEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 360;

    garden pea

                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 867.5; DB 2;
; Pred. No. 5.8e-62;
60; Mismatches 116;
                 1.1e - 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6a-hydroxymaackiain methyltransferase (BC 2.1.1.-)
                             55; Mismatches
65.6%; Score 1237.5; 66.5%; Pred. No. 1.1e
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Db

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Outchyltransferase (EC 2.1.1.-) - maize
C.Species: Zea mays (maize)
C.Species: Zea ways (maize)
C.Species: Zea ways (maize)
C.Species: Zea.May 1985
R.Jeld, B.M.; Wang, H.; John, I.; Wurtele, E.S.; Colbert, J.T.
B.Held, B.M.; Wang, H.; John, I.; Wurtele, E.S.; Colbert, J.T.
B.Held, B.M.; Wang, H.; John, I.; Wurtele, E.S.; Colbert, J.T.
A.Piant Physiol. 102, 1001-1008, 1193
A.Reference number: J02268; MUID:94105316; PMID:8278520
A.Reference number: J02268
A.Molecule type: MRNA
A.Residues: 1-364 cHEL>
A.Residues: 1-364 cHEL>
A.Rorosa-references GB:114063; NID:9404069; PIDN:AAA18532.1; PID:9404070
C.Superimental source: root, cv. NKH31
C.Superimental source: root, cv. NKH31
C.Superimental sources methyltransferase
C.Keywords: methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 VSILQVPPTKTRQVQSLMRYLAHNGFPBIVRI-----HDNIBAYALTAASELLV--KSSB 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 LSKVHLHPSRVSSLRRLMRVLTTTNVFGTQPLGGGSDDDSEPVYTLTPVSRLLIGSQSSQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 LAQTPLAAMVLDPTIVSPFSELGAWFQHELPDPCIFKHTHGRGIWELTKDDATFDALVND 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 NLSGSNNLTFVGGDMFKCIPKADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVV 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            catechol O-methyltransferase homolog - Monterey pine C;Species: Pinus radiata (Monterey pine) C;Decies: Pinus radiata (Monterey pine) C;Decies: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-Aug-1999 C;Accession 709600 R;Wagner, A.; Malden, A.; Narayan, R.; Walter, C. submitted to the EMBL Data Library, September 1996 A;Reference number: Z16762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 AMACDSQML-NLAFRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSLAPMVEYFLEPNCQGAWNQLKRWVHEE--DLTVFEVSLGTPFWDFINKDPAYNKSFNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VIDTVINENKDERQVTELKLLMDVHWACIINGKERKEEDWKKLFMEAGFQSYKISPFTGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MASSLANGRKASEIFQGQALLYKHLLGFIDSKCLKWMVELDIPDIIHSHSHGQPITFSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MELSPNNSTDOS-LLDAOLELWHTTFAFMKSMALKSAIHLRIADAI--HLHGGAASLSQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 KAPTHTDVQFIAGDMFESIPPADAVLLKSVLHDWDHDDCVKILKNCKKAIPPREAGGKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                        32.1%; Score 606; DB 2; Length 36 35.9%; Pred. No. 5.8e-41; cive 74; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U70873; NID:g1568663; PID:g1568664
A;Experimental source: tissue-type male cone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.1%; Score 529.5; DB 2; 33.5%; Pred. No. 8.6e-35; ive 69; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: T09600
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: O-methyltransferase C;Keywords: methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 32.1
Best Local Similarity 35.9
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 28.1
Best Local Similarity 33.5
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSLIEIYP 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:||:||
357 RSIIEVYP 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
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R,Gregersen, P.L.; Christensen, A.B.; Sommer-Knudsen, J.; Collinge, D.B.
Plant Mol. Biol. 26, 1797-1806, 1994
A,Title: A putative O-methyltransferase from barley is induced by fungal pathogens and A,Reference number: S52015; MUID:95161704; PMID:7858218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A/Cross-references: EMBL:X77467
R/Gregersen, P.L.; Christensen, A.B.; Sommer-Knudsen, J.; Collinge, D.B.
Submitted to the EMBL Data Library, February 1994
A/Description: A novel putative O-methyltransferase from barley is induced by fungal EA/Accession: S41949
A/Accession: S41949
A/Accession: S41949
A/Accession: S41949
A/Residues: 1-315,'H', 117-390 (GRW)
A/Residues: 1-315,'H', 117-390 (GRW)
A/Cross-references: EMBL:X77467; NID:g453243; PIDN:CRA54616.1; PID:g453244
C;Superfamily: O-methyltransferase
C;Keywords: methyltransferase; S-adenosylmethionine
  LAFRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFV 241
                                    GGDMFKCIPKADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKD 301
                                                                                                                                          115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 IHPNKLPYLPRLMKMLAAAGIFTAEDVPATVGDGEPTTLYHLNAVSRLLVDDASVNGGAS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 NLSGSNNLTFVGGDMFKCIPKADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVV 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291 VIDTVINENKDERQVTELKLLMDVHMACIINGKERKEEDWKKLFMEAGFQSYKISPFTGY 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 LAPMVEYFLEPNCQGAWNQLKRWVHEBDL----TVFEVSLGTPFWDFINKDPAYNKSFNE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GISSHGTVBFVAGDWMBFVPPAEAVLLKYVLHNWSDQDCVKILTRCREAISPGEKAGKVI 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84
                                                                                                                                                                                                                                                 catechol O-methyltransferase (EC 2.1.1.6) - barley
C;Species: Hordeum vulgare (barley)
C;Date: 28-Oct.1996 #sequence_revision 07-Feb-1997 #text_change 05-May-2000
                                                                                                                                                                                                                   ERQVTELKLLMDVHMACIINGKERKEEDWKKLFMEAGFQSYKISPFTGYLSLIEIYP 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 VPPTKTRQVQSLMRYLAHNGFFEIVRIHDNI-----EAYALTAASELLVKSSEL---S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 AMACDSOML-NLAFRDCNWVFEGLESIVDVGGGTGTTAKIICEAFPKLKCMVLERPNVVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 NNGRKASEIFQGQALLYKHLLGFIDSKCLKWMVELDIPDIIHSHSHGQPITFSELVSILQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 652.5; DB 2; Length 3; Pred. No. 1.2e-44; 67; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.6%;
39.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 39.1%
Matches 144; Conservative
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RSLIEVOP 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-390 <GRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S52015
                                                       184
                                                                                                                                                                                                                302
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                                                                                                         242
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Gaps

43;

Indels

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Qy 297 NEMKDBRQVTELKLIAMD-VHMACIINGKERKEEDWKKLFWEAGFQSYKISPFT 348 Db 312 GENKKTMIVDERDEKLEHVRIALDWVMMAHTSTGKERTIKEWDFVLKEAGFARYEVRDID 371 Qy 349 GYLLIEIY 357 Db 372 DVGSLIIAY 380 RESULT 9 T04952 C,Species: Arabidopsis thaliana (mouse-ear crees) C,Dete: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 24-Nov-1999 C,Accession: T04962 C,Accession: T04962 C,Accession: T04962 C,Accession: T04962 C,Accession: T04962 C,Accession: T04962 A,Roccession: T04962 C,Genetics: Columbia; BAC clone T1205 C,Superfamily: O-methyltransferase	Query Match 25.7%; Score 485; DB 2; Length 325; Best Local Similarity 32.3%; Pred. No. 2.6e-31; Matches 113; Conservative 64; Mismatches 115; Indels 58; Gaps 8; 21 LYKHLIGFIDSKCLKWAWUELDIPDIHSHENGDITFSELVSILQVPPTKTRQVSLMRY 80; 12 INKRYPGFADIAAAKCAIDLKIPEAIENHPSSQPVILSELSSAVSASPSHLRRIMRF 75; Qy 81 LAHNGFFELVRIHDNI-EAYALTAASELLVKSSELSLAPMVEYFLEPNCQGAWNQLKRWV 139; Db 76 LVHQGLFKEVPTKDGLATGYTNTPLSRRMMITK	308 IKLIMDVHAACIINGKERKEEDWKKLFAAGFOSYKISPTGYLSIIIY 357
1 MASSLNNGRKAS	T12J5.30 - Arabidopsis thaliana se-ear cress) on 23-Apr-1999 #text_change 26-Aug-1999 Hudson, S.; Hoheisel, J.; Mewes, H.W.; tabase, February 1999 mbia; BAC clone T12J5 ore 527; DB 2; Length 382; ed. No. 1.4e-34;	POGCALLYKHLLGFIDSKCLKMWVBLDIPDI AKASLDIWKYVGFADIAAAKCAIDLKIPES QSLMRYLAHNGFEIVRIHDNI-BAYALTAR QSLMRYLAHNGFEIVRIHDNI-BAYALTAR WNQLKRWWHEDDITVEVSLGTPFWDI

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expression of alfalfa isoliquiritigenin
        206 DVGGGTGATVAMIVSKYPSIKGINFDLPHVIGDAPTYPGVEHVGGDMPASVPKADAIFMK 265
                                                                        259 LVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVTELKLLMDVHM-A 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----LMNQDKVLMESWYHLKD 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 LIV-----FEVSLGTPFWDFINKDPAYNKSFNEAMACDSOMLNLAFRDCNWVFEGLESIV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVLLK 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 LVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVTELKLLMDVHM-A 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               266 WICHDWSDEHCLKFLKNCYEALPA---NGKVIIAECILPEAPDTSLATKNTVHVDIVMLA 322
                                                                                                                                                                                                                                                                                               catechol O-methyltransferase (BC 2.1.1.6) - common tobacco C;Species: Nicotiana tabacum (common tobacco) C;Accession: S36404 sequence_revision 10-Nov-1995 #text_change 05-May-2000 R;Legrand, M. submitted to the EMBL Data Library, August 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isoliquiritigenin 2'-O-methyltransferase - alfalfa
C;Species: Medicago sativa (alfalfa)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T09617
R;Maxwell, CA.; Harrison, M.J.; Dixon, R.A.
Plant 4, 971-981, 1993,
A;Title: Molecular characterization and expression of alfalfa isoliquiritige
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Reference number: 216778; MUID:94108491; PMID:8281189
A;Accession: T09617
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-372 <MNX>
A;Residues: 1-372 <MNX>
A;Cross-references: EMBL:L10211; NID:9289126; PIDN:AAB48059.1; PID:91843462
                                                                                                 266 WICHDWSDEHCLKFLKNCYEALPA---NGKVIIAECILPEAPDTSLATKNTVHVDIVMLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 LKMMVBLDIPDIIHSHSHGQPITFSELVSIL----QVPPTKTRQVQSLMRYLAHNGFFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKSALELDLLELMAKAGPGAAISPSELAAQLSTQNPEAPVILDRMLRLLATYSVLNCTLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89 IVRIHDNIBAYALTAASELLVKSSE-LSLAPMVEYFLEPNCQGAWNQ----LKRWVHBED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: 836403
A;Accession: 836404
A;Accession: 836404
A;Residues: 1-364 <LEG>
A;Cross-references: EMBL:X74453; NID:g396590; PID:g396591
C;Superfamily: O-methyltransferase; S-adenosylmethionine
                                                                                                                                                         318 CIINGKERKEEDWKKLFMEAGFQSYKISPFTGYLSLIEI 356
                                                                                                                                                                                               HNPGGKERTEKEFEALAKGAG-----FIGFARLVAL 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318 CIINGKERKEEDWKKLFMEAGFQSYKISPFTGYLSLIEI 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----FTGFARLVAL 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 20.5%; Score 386.5; DB 2; Best Local Similarity 30.1%; Pred. No. 2.4e-23; Matches 102; Conservative 64; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HNPGGKERTEKEFEALAKGAG
                                                                                                                                                                                               323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36
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A;Cross-references: EMBL:AF033496; NID:g2921303; PIDN:AAC12715.1; PID:g2921304
A;Experimental source: strain B73
C;Genetics:
A;Gene: SEP1
A;Map position: 2
C;Superfamily: O-methyltransferase
                                                                                                                                                                                                                                                                                                                                                               128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 M-ACDSQMLNLAFRDCNWVFEGLESIVDVGGGTGIT--AKIICEAFPKLKCMVLERPNVV 229
                                                                                                                                                                                                                                                                                                                  72 RQVQSLMRYLAHNGFFEIVRIHDNIEAYALTAASELLV------KSSELSLAPMVEY 122
                                                                                                                                                                                                                                                                                                                                                                                                 PLEPNCQGAWNQLKRWVHE-----EDL---TVFEVSLGTPFWDFINKDPAYNKSFNEA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                             176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENLSGSN-NLTFVGGDMFKCIPKADAVLLKLVLHNWNDNDCMKILENCKBAISGESKTGK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVVIDTVINENKDERQVTELKLLMDVHMACIINGKERKEEDWKKLFMEAGFQSYKISPFT 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89 IVRIHDNIEAYALTAASELLVKSSE-LSLAPMVEYFLEPNCQGAMNQ----LKRWVHEED 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 LIV-----FEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVFEGLESIV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVLLK 258
                                                                                                                                                                                                                                                                              68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     catechol O-methyltransferase (EC 2.1.1.6) - common tobacco catechol O-methyltransferase (EC 2.1.1.6) - common tobacco cyspecies: Nicotiana tabacum (common tobacco)
c;Spacies: O9-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-May-2000
C;Accession: S36403
R;Degrand, M.
A;Reference number: S36403
A;Reference number: S36403
A;Recession: S36403
A;Rocession: S36403
A;Rocession: S36403
A;Rocession: S36403
C;Superfamily: O-methyltransferase; Sadenosylmethionine
C;Superfamily: O-methyltransferase; S-adenosylmethionine
                                                                                                                                                                                                                                                                                                                                         129 YIE-----AGIGLABWPKRDVVISPFEELHGATLFHESMG------SLDADFHDMASBA
                                                                                                                                                                                                                                                           12 SEIFQGQALLYKHLLGFIDSKCLKWMVELDIPDIIHSHSHGQPITFSELVSILQVPPTKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 LKWMVELDIPDIIHSHSHGQPITFSELVSIL-----QVPPTKTRQVQSLMRYLAHNGFFE
                                                                                                                                                                                           Gaps
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                                                                                                                                                                                             40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 364;
                                                                                                                                                  DB 2; Length 363; 1.6e-26;
                                                                                                                                                                                             Indels
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                                                                                                                                                                                           Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: O-methyltransferase ... Keywords: methyltransferase; S-adenosylmethionine
                                                                                                                                                22.6%; Score 426;
larity 31.4%; Pred. No. 1
Conservative 70; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                   Similarity
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Best Local Simi
Matches 116;
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Matches
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8

Gaps

37;

88

143

265

2'-0-1

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caffeate O-methyltransferase (BC 2.1.1.68) - alfalfa
C;Species: Medicago sativa (alfalfa)
C;Species: Medicago sativa (alfalfa)
C;Species: Medicago sativa (alfalfa)
C;Species: Medicago sativa (alfalfa)
C;Species: Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T06673
R;Gowri, G; Bugos, R.C; Campbell, W.H.; Maxwell, C.A.; Dixon, R.A.
Plant Physiol. 97, 7-14, 1991
A;Title: Molecular cloning and expression of alfalfa S-adenosyl-L-methionine: caffe
A;Reference number: 216815
A;Reference number: 216815
A;Status: preliminary; translated from GB/BMBL/DDBJ
A;Status: preliminary; translated from GB/BMBL/DDBJ
A;Status: preliminary; translated from GB/BMBL/DDBJ
A;References: BRNA
A;References: BRNA
A;References: Subspecies sativa, cultivar Apollo
C;Function: A;Pethway: lignin biosynthesis
C;Superfamily: O-methyltransferase; S-adenosylmethionine
                                                                                                                                                                 LLKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVTELKLLMDVH 315
                                                                                                                                                                                           LTDAVLDGGVPFNKAYGMTAFEYHGTDPRFNKVFNRGMSDHSTMTMKKILLEDYKGFEGLN 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VRIHDNIBA---YALTAASELLVKSSE-LSLAPMVEYFLEPNCQGAWNQ----LKRWVHE 141
                                                                                                   SIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 İKSALELDILETİAKAGPGAQİSPIETAS--QLPTINPDAPVMLDRMLRLACYTILTCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BDLTV-----FEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVFEGLES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --NLMNQDKVLMESWYHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 IVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 LKWMVELDIPDIIHSHSHGQPITFSELVSILQVPPTKTRQVQSLMRYLAHNGFFEI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.1%; Score 379.5; DB 2;
31.4%; Pred. No. 8.9e-23;
live 63; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           316 M-ACIINGKERKEEDWKKLFMEAGFOSYK 343
                                                                                                                                                                                                                                                                                              316 MLAHNPGGKERTEKEFEALAKGAGFTGFR 344
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Best Local Similarity 31.49
Matches 106; Conservative
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712259
O-diphenol-O-methyltransferase (BC 2.1.1.-) - pepper
C.Species: Capsicum annuum (pepper)
C.Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 11-Jan-2000
C.Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 11-Jan-2000
C.Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 11-Jan-2000
C.Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 11-Jan-2000
R.Date: 05-Nov-1999 #sequence_revision
C.Date: 05-Nov-1999 #text_change 11-Jan-2000
R.Date: 05-Nov-1999 #sequence_revision
R.Date: 05-Nov-1999 #text_change 11-Jan-2000
R.Date: 05-Nov-1999 #sequence_revision
R.Date: 05-Nov-1999 #sequence_revision
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R.Date: 05-Nov-1999 #text_changerase
R.Date: 05-Nov-1999 #te
                                                        of isoliquiritigenin (2',4,4'-trihydroxychalcd is the most potent of the nod-gene-inducing fl
                                                                                                                                                                                                                                                                                                                                                                                                                  SDLPNRLDRMLRLLA--SYSVLTSTTRTİEDGGAERVYGLSMVGKYLVPDESRGYLASFT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MLNLAFRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNL 238
                                                                                                                                                                                                                                                                                                                                                                      ----QVQSLMRYLAHNGFFEIVRIHDNIE-----AYALTAASELLV-KSSELSLAPMV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 NKDERQVTELKLLMDVHWACIINGKERKEEDWKKLFMEAGFQSYKIS--PFTGYLSLIEI 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BPNTSEESKLVSTLDNLMFITVGGRERTEKQYEKLSKTSGFSKFQVACRAFNS-LGVMEF 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BEDLTV-----FEVSLGTPFWDFINKDPAYNKSFNEAMACDSOMLNLAFRDCNWVFPGLE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EYFLEPNCQGAWNQLKRWVHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAM--ACDSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TFVGGDMFKCI PKADAVLLKLVLHNWNDNDCMKILENCKBAISGBSKTGKVVVIDTVINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EHVGGDMFASVPQGDAMILKAVCHNWSDEKCIEFLSNCHKAL---SPNGKVIIVEFILPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 FFEIVRIHDNIEAYALTAASELLVKSSE-LSLAPMVEYFLEPNCOGAWNQ----LKRWVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 LKWMVELDIPDIIHSHSHGQPITFSELVSILQVPPTKT------RQVQSLMRYLAHNG
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                     Length 372;
                                                                                                                                                                         20.4%; Score 384; DB 2; Length 372
llarity 28.5%; Pred. No. 4e-23;
Conservative 77; Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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A;Experimental source: subspecies sativa; cultivar Apollo C;Function:
A;Description: methylates the 2'-hydroxyl of isoliquiritig A;Note: 4'-dihydroxy-2'-methoxychalcone is the most pote C;Superfamily: O-methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.3%; Score 383.5; DB 2; 31.3%; Pred. No. 4.1e-23; ive 60; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 31.3'
Matches 103; Conservative
                                                                                                                                                                                                     Similarity
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Matches 103;
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Gaps

35;

83 93 196

203 256 320

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

November 10, 2003, 01:53:20 ; Search time 23 Seconds (without alignments) 731.981 Million cell updates/sec

US-09-868-547-4 1886 1 MASSLANGRKASEIFÇGQAL......FQSYKISPFTGYLSLIEIYP 358 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

	cription	100	zea mavs	coptis	Osll87 coffea cane	Q9fk25 arabidopsis	Q9fqy8 capsicum an		P59049 chrysosplen		Q42653 chrysosplen	O81646 capsicum ch	Q9xgw0 ocimum basi	Q00763 populus tre	043046 populus kit	043609 prunus dulc	043047 populus kit	Q9xqv9 ocimum basi	Q41086 populus tre	eucalypt		O23760 clarkia bre	zinnia e	-	^,	01	-	10	5528	2712	a	20	46597 homo	056 gall
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ALIGNMENTS

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                                                                                               137
                                                                                                         196
                                                                                                                                                    IVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVL 256
                                                                                                                                                                                                :||||||||| : | ||||||::
188 LVDVGGGTGTAVRNIANAFPHIKCTVYDLPHVIADSPGYSEVHCVAGDMFKFIPKADAIM 247
                                                                                                                                                                                                                            257 LKLVLHNWNDNDCMXILENCKEAISGESKTGKVVVIDTVINENKDERQVTELKLLMDVHM 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 QALLYKHILGFIDSKCLKWMVELDIPDIIHSHSHGQPITFSELVSILQVPPTKTRQVQSL
                                                            11 QAKLWNFIYGFAESLVLKCAVQLDLANII--HNSGTSMTLSELSSRLPSQPVNEDALYRV
                                                                                         MRYLAHNGFFEIVRIHDNIEAYALTAASELLUVKSSELSLAPMVEYFLEPNCQGAWNQLKR
                                                                                                                                      138 WVHEEDLIVFEVSLGTPFWDFINKDPAYNKSFNBAMACDSQMLNLAF-RDCNWVFBGLBS
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
                           ..
    Length 347;
             ; Pred. No. 5.2e-44;
70; Mismatches 132; Indels
                                                                                                                                                                                                                                                                              358
                                                                                                                                                                                                                                                                                                    346
                                                                                                                                                                                                                                                                                       305 MLNTGGKERTEESWKKLIHDAGYKGHKITQITAVQSVIEAYP
                                                                                                                                                                                                                                                                          317 ACIINGKERKEEDWKKLFMEAGFQSYKISPFTGYLSLIEIYP
  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996 (Rel. 33, Last sequence update) 01-OCT-1996 (Rel. 34, Last annotation update) O-methyltransferase ZRP4 (EC 2.1.1.-) (OMT).
                                                                                                                                                                                                                                                                                                                                                          364 AA
33.7%; Score 636.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001601; Methyltransf.
InterPro; IPR001077; O_Metransf2.
                                                                                                                                                                                                                                                                                                                                                                              Created)
              38.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L14063; AAA18532.1; -.
PIR; JQ2268; JQ2268.
                       133; Conservative
                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                            (Rel. 33, (Rel. 33, 1) (Rel. 34, 1)
             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MaizeDB; 63528;
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01-FEB-1996
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           Best Local
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This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                     61 VSILQVPPTKTRQVQSLMRYLAHNGFFEIVRI-----HDNIEAYALIAASELLV--KSSE 113
                                                                                                                                                                                                                                                                                                                                 58 LSKVHLHPSRVSSLRRLMRVLTTTNVFGTQPLGGGSDDDSEPVYTLTPVSRLLIGSQSSQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 LSLAPMVEYFLEPNCQGAWNQLKRWVHEE--DLTVFEVSLGTPFWDFINKDPAYNKSFNE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                   118 LAQTPLAAMVLDPTIVSPFSELGAWFQHELPDPCIFKHTHGRGIWELIKDDATFDALVND 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231 NLSGSNNLTFVGGDMFKCIPKADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVV 290
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                                                                                                                                                                                                            1 MASSLANGRKASEIFQGQALLYKHLLGFIDSKCLKWMVELDIFDIHSHSHGQPITFSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 AMACDSOML-NLAFRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 KAPTHTDVQFIAGDMFESIPPADAVLLKSVLHDWDHDDCVKILKNCKKAIPPREAGGKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIDTVINENKDERQVTELKLIMDVHMACIINGKERKEEDWKKLFMEAGFQSYKISPFTGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 IINMVVGAGPSDMKHKEMQAIPDVYI-MFINGMERDEQEMSKIFSEAGYSDYRIIPVLGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
3'-hydroxy-N-methyl-(S)-coclaurine 4'-0-methyltransferase
GEC 2.1.1.116) (S-adenosyl-methionine:3'-hydroxy-N-methylcoclaurine
4'-0-methyltransferase) (4'-0WT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3'-hydroxy-N-methyl-S)-coclaurine = 8-adenosyl-L-homocysteine + (8)-reticuline.
PATHWAY: CARRIES OUT A STEP IN THE CONVERSION OF 3'-HYDROXY-N-METHYLCOCLAURINE TO RETICULINE, AN IMPORTANT INTERMEDIATE IN
                                                                                                                                                                                                                                                       1 MELSPNNSTDQS-LLDDAQLELWHTTFAFMKSMALKSAIHLRIADAI--HLHGGAASLSQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.
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                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20390108; PubMed=1081648; Sato F.; Morishige T., Tsujita T., Yamada Y., Sato F.; Morishige T., Tsujita T., Yamada Y., Sato F.; Morlecular characterization of the S.adenosyl-L-methionine: 3'-hydroxy-N-methylcoclautine 4'O-methyltransferase involved isoquinoline alkaloid biosynthesis in Coptis japonica."; J. Stol. Chem. 275:23398-234605(2000). THE METHYL GROUP TO T. HYDROXYL GROUP OF 3'-HYDROXYN-N-METHYLCOCLAURINE TO FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: Homodimer.
-!- SIMILARITY: BELONGS TO THE METHYLITRANSFERASE SUPERFAMILY.
                                                                                                                         Length 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coptis japonica (Japanese goldthread).
Wakaryota, Viridiplantae; Streptophyta; Embryophyta; Trache Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales; Ranunculaceae; Coptis.
                                                                       FB8AD93AD5A6611D CRC64,
                                                                                                                  32.1%; Score 606; DB 1; L. 35.9%; Pred. No. 1.6e-41; .ive 74; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYNTHESIZING ISOQUINOLINE ALKALOIDS.
                       Pfam, PF00891, Methyltransf 2, 1.
Transferase, Methyltransferase.
SEQUENCE 364 AA, 39583 MW, FB.
InterPro; IPR000051; SAM_bind.
                                                                                                                                                          Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C 2.1.1.116) (S-aucilon-O-methyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        357 RSIIEVYP 364
                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              351 LSLIEIYP
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                                                                                                                    Query Match
                                                                                                                                            Local
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40MT_COPJA
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192 EGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 QGIDSLVDVGGGNGTTVKAISDAFPHIKCTLFDLPHVIANSYDLPNIERIGGDMFKSVPS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADAVLIKLVLHNWNDNDCMKILBNCKEAISGESKTGKVVVIDTVINENKDERQVTELKLL 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KRWVHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSOMLNLAF----RDCNWVF 191
the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 KAQAHVWKIIYGFADSLVLRCAVBLGIVDIJDNNN--QPMALADLASKLPVSDVNCDNLY 70
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"Complete cDNA sequence of a caffeic acid O-methyltransferase from
"Coffea canephora fruit.",
Submitted (DEC-2001) to the EMBL/GenBank/DBBJ databases.
-!- FUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid
and of 5-hydroxyferulic acid to shapic acid. The resulting
products may subsequently be converted to the corresponding
alcohols that are incorporated into lighins.
-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihydroxy-trans-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-trans-
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15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last nontation update)
15-SEP-2003 (Rel. 42, Last sequence update)
Caffeic acid 3-O-methyltxansferase (EC 2.1.1.68) (S-adenosysl-L-methionine:caffeic acid 3-O-methyltransferase) (COMT) (CAOMT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 587.5; DB 1; Length 350; Pred. No. 4.7e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               547835EBCDEF9182 CRC64;
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                                                                                                                                                                                                                                                                                            Interpro; IPR001601, Methyltransf.
Interpro; IPR001077; O_Metransf2.
                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00891; Methyltransf 2; 1.
Transferase; Methyltransferase.
SEQUENCE 350 AA; 38775 MW; 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cinnamate.
PATHWAY: Lignin biosynthesis.
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Bukaryota, Viridiplantae, Strepto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.2%;
                                                                                                                                                                                                                                                                 EMBL; D29812; BAB08005.1; -.
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TISSUE=Fruit, and Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           257 LKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVTELKLLMDVHM 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 LINILADGGVERLYGLAPVCKFLTKNADGVSMAPIL------LMNQDKVLMESWYHL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 BDLTV----FEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVFFGLES 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 KDAVLDGGIPFNKAYGMTAFEYHGTDPRFNKVFNQGMSNHSTITMKKILEVYRGFEGLKT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 IVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVL 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 VVDVGGGTGATLNMIISKYPTIKGINFELPHVVEDAPSHSGVEHVGGDMFVSVPKGDAIF 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 MKWICHDWSDDHCRKLLKNCYQAL---PDNGKVILAECVLPEAPDTSLATONVVHVDVVM 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 LKWMVELDIPDIIHSHSHGQPIIFSELVSILQVP---PTKTRQVQSLMRYLAHNGFFE-- 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 LKSAIELDLLELIAKAGPGAYVSPSBLAA--QLPTHNPEAPIMLDRILRLLATYSVLDCK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
45-SEP-2003 (Rel. 42, Last annotation update)
60-ercetin 3-0-methyltransferase 1 (EC 2.1.1.76) (AtOM11) (Flavonol 3-0-methyltransferase 1) (Caffeic acid/5-hydroxyferulic acid 0-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89 IVRIHD-NIE-AYALTAASBLLVKSSB-LSLAPMVEYFLBPNCQGAWNQ----LKRWVHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiphantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
-:- SIMILARITY: Belongs to the methyltransferase superfamily. Family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. C24; TISSUE=Leaf;
MEDLINE=98007865; PubMed=3349713;
Zhang H., Wang J., Goodman H.M., "An Arabidopsis gene encoding a putative 14-3-3-interacting protein,
                                                                                                                                                                                          entil...

"R smEL, AF454631, AAN03726.1; -.

"R mEL, AF454631, AAN03726.1; -.

"R mEL, AF454631, AAN0372.1; -.

"R milerPro: IPR001077; O Metransf2.

"DR InterPro: IPR001077; O Metransf2.

"DR InterPro: IPR001077; O Metransf2.

"DR InterPro: IPR008091; Methyltransfe.

"DR InterPro: IPR00891; Methyltransf2.

"DR Pfam; PF00891; Methyltransf2.

"DR Pfam; PF00891; Methyltransf2.

"DR Pfam; PF00891; Methyltransf2.

"DR Pfam; PR00891; Methyltransf2.

"DR Pfam; PR00891; Methyltransf2.

"DR Pfam; PR00891; Methyltransf2.

"DR Pfam; PR00891; Methyltransf2.

"O'NFLICT 230 230 8. -> P (IN REF. 1; AAN03726).

"O'NFLICT 230 28 K -> R (IN REF. 1; AAN03726).

"O'NFLICT 230 28 K -> R (IN REF. 1; AAN03726).

"O'NFLICT 230 28 K -> R (IN REF. 1; AAN03726).
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les 122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.8%; Preu. ....
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    COMT subfamily.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arch. Blochem. Blophys. 375:385-388(2000).

-!- FUNCTION: Methylates OH residues of flavonoid compounds. Substrate preference is quercetin > myricetin.> luteolin. Dihydroquercetin is not a substrate. Has an optimal pH of 7.5.

-!- CATALYTIC ACTIVITY: Sadenosyl-L-methionine + 3,5,7,3',4'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SUBUNIT: Monomer.
-i- SIMILARITY: Belongs to the methyltransferase superfamily. Family
                                                                                                              Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
                                                                                                                                                                                                                                                         STRAIN=cv. Columbia;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
"RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
SSP consortium (Salk/Stenford/PGEC).";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20166962; PubMed=10700397; Muzac I., Wang J., Anzellotti D., Zhang H., Ibrahim R.K.; "Functional expression of an Arabidopsis cDNA clone encoding a flavonol 3'-0-methyltransferase and characterization of the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5,7,3',4'-tetrahydroxyflavone.
BNZYME REGULATION: Does not require magnesium. Completely
inhibited by 5 mM of either NiSO4 or p-chloromercuribenzoate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,5,7,3',4'-
pentahydroxyflavone = S-adenosyl-L-homocysteine + 3-methoxy-
                                                                                                                                              "Structural analysis of Arabidopsis thaliana chromosome 5. VI. Sequence features of the regions of 1,367,185 bp covered by 19 physically assigned Pl and TAC clones."; DNA Res. 5:203-216(1998).
                                                                                                                                                                                                                                                                                                                                                                                                               Delseny
caffeic acid/5-hydroxyferulic acid O-methyltransferase.";
Biochim. Biophys. Acta 1353:199-202(1997).
                                                                                                                                                                                                                                                                                                                                                 [4]
SEQUENCE OF 285-363 FROM N.A.
SEQUENCE OF Columbia; TISSUE-Green siliques;
STRAIN-cv. Columbia; TISSUE-Green siliques;
Raynal M., Grellet F., Laudie M., Meyer Y., Cooke R., De
Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B4380028D89C43DC CRC64;
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D -> N (IN RE
E -> V (IN RE
T -> S (IN RE
V -> C (IN RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATHWAY: Phenylpropanoid pathway.
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EMBL, A8013387; BAB11578.1; --
EMBL, AY062837; AA13219.1; --
EMBL, 227062; CAA81580.1; --
EMBL, 227062; CAA81580.1; --
InterPro; IPR011601; Methyltransf,
InterPro; IPR001001; Ometransf2.
InterPro; IPR0010051; SM bind.
Pfam; PF00991; Methyltransf2.
                                                                          STRAIN=cv. Columbia;
MEDLINE=98403884; PubMed=9734815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION, AND CHARACTERIZATION
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                                                                                                                                                                                                                     [3]
SEQUENCE FROM N.A.
STATES COlumbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2. COMT subfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348
363 AA;
                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
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Score 390.5; DB 1; Length 363; Pred. No. 3.8e-24;

20.7%;

.Query Match Best Local Similarity

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12;
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                                                                                                                                                                                                                                                                                                                                                                       -----LTSYSVLTCSNRKLSGDGVERIYGLGPVCKY-LTKNEDGVSIAALCLMNQDKV 133
                                                                                                                                                                                                                                                                                         -----LAPMVEYFLEPNCQGA-----WNQ--- 134
                                                                                                                                                                                                  81
                                                                                            34 LKWMVELDIPDIIHSHSHGQPITFSELVSILQVPPTKTRQVQSLMRYLAHNGFFEIVRIH 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lee B.-H., Choi D., Lee K.-W., "Isolation and characterization of o-diphenol-O-methyltransferase cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA from Capsicum annuum.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid and of 5-hydroxyferulic acid to sinapic acid. The resulting products may subsequently be converted to the corresponding alcohols that are incorporated into lignins.
-!- CATALYTIC ACTIVITY: S_adenosyl-L-methionine + 3,4-dihydroxy-trans-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY: Fruit. Not expressed in leaf.
DEVELOPMENTAL STAGE: Expression increases during fruit development
but decreases during ripening.
SIMILARITY: Belongs to the methyltransferase superfamily. Family
                                                                                                                                                                                             -----RILRL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 KGFEGLTSLVDVGGGIGATLKMIVSKYPNIKGINFDLPHVIEDAPSHPGIEHVGGDMFVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|| ||: :| :| |: |: | |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |:
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                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=cv. Chungyang, TISSUE=Root,
Kim K.-W., Lee S.-W.;
"Isolation and characterization of caffeic acid O-methyltrasferase
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, lamiids, Solanales, Solanaceae, Capsicum.
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              . 69
                                                                                                                                                                                   36 LKSALELDLLEIM--AKNGSPMSPTEIASKL---PTKNPEAPVMLD-
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    69; Mismatches
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J. Plant Biol. 41:9-14(1998).
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106; Conservative
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                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BEDLIV-----FEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVFEGLE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAV 255
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"Molecular and biochemical characterization of caffeic acid O-
"methyltransferase from Catharanthus roseus ";
Submitted Marazoul) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid
and of 5-hydroxyferulic acid to sinapic acid. The resulting
products may subsequently be converted to the corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alcohols that are incorporated into lignins. 3,4-dihydroxy-trans-CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3,4-dihydroxy-transcinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-trans-
                      in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKWMVBLDIPDIIHSHSHGQPITFSBLVSILQVPPTKT------RQVQSLMRYLAHNG
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, lamilds, Gentianales, Apocynaceae, Rauvolfioideae, Vinceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 PPEIVRIHDNIEAYALTAASELLVKSSE-LSLAPMVEYFLEPNCQGAWNQ----LKRWVH
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15-SEP-2003 (Rel. 42, Last sequence update)
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EMBL; AP21216; AAG43822.1;

EMBL; AP21216; AAG43822.1;

InterPro; IPR001601; Methyltransf2.

R InterPro; IPR001001; SAW bind.

R Pfam; PF00891; Methyltransf2; 1.

Pfam; PF00891; Methyltransf6rase.

W ijgnin biosynthesis; Transf6rase;

Over ICT (IN REF. 2).

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                                                                                                              send an email to license@isb-sib.ch).
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PATHWAY: Lignin biosynthesis.
SIMILARITY: Belongs to the methyltransferase superfamily. Family 2. COMT subfamily.
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Quercetin 3-O-methyltransferase 1 (EC 2.1.1.76) (Flavonol 3-O-
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Spermatophyta; Magnoliophyta; eudicotyledons, core eudicots;
Saxifragales; Saxifragaceae; Chrysosplenium.
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Lignin biosynthesis; Transferase; Methyltransferase
SEQUENCE 363 AA; 39785 MW; 700D420F98A52E35 CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 383.5; DB 1;
Pred. No. 1.4e-23;
71; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLLMDVHM-ACIINGKERKEEDWKKLFMEAGFOSY 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     343 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AY028439, AAX20170.1; -.
InterPro, IPR001601; Methyltransf.
InterPro, IPR001077; O Metransf2.
InterPro, IPR000051; SĀM Dind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 29.35
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae,
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106; Conservative
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                                                                                                                                                                                                                                                                                                          2. COMT subfamily
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28-FEB-2003
15-SEP-2003
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Best Local S
Matches 106
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Q42653;
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                                                                                                                                           CC 5,7,3',4'-
Dentahydroxyflavone = S-adenosyl-L-methionine + 3,5,7,3',4'-
Dentahydroxyflavone = S-adenosyl-L-homocysteine + 3-methoxy-
S,7,3',4'-terrahydroxyflavone.
CC -!- FATHWAY: Phenylpropanoid pathway.
CC -!- MISCELLANBOUS: The Vmax value for flavonoid compounds is two to
threefold higher for OWT1 than for OWT2.
CC -!- GNMILARITY: Belongs to the methyltransferase superfamily. Family
C -!- CAUTION: It is not sure if OWT1 and OWT2 are really encoded by two
different genes or if they represent cloning artifacts.
CC -!- CAUTION: In they represent cloning artifacts.
DR InterPro: IPRO01601; Methyltransf.
R InterPro: IPRO01601; Methyltransf.
R InterPro: IPRO01601; Methyltransf.
R Pfem: PF00891; Methyltransf.
W Methyltransferase: Transf.
W Methyltransferase: Transf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 VRIHDNIEAYALTAASELLVKSSE-LSLAPWVEYFLEPNCQGAWNQ----LKRWVHEEDL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 TV----FEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVFEGLESIVD 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 VLDGGIPFNKAYGMSSFEYHGTDPRFNKVFNRGMSDHSTITMKKVFQAYQGFQGLFSLVD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 VGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVLLKL 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINBNKDERQVTBLKLLMDV-HMAC 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : |:|:| |:|:|| |:|:
243 ICHDMSDEHCLKLLKNCYDAL---PNNGKVILAECILPEVPDSSLATKGVVHIDVITVAH 299
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two
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 LKSAIBLDLLEII----RGODTCMSPTBIASHLPTTNPDAPAMVDRILRLLSCYSVVTCS
                             phenylpropanoid
                                                                                                                        not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae, Medicago.
               -!- FUNCTION: Methylates OH residues of flavonoid and phenylpropano compounds and shows a higher affinity for flavonoid than phenylpropanoid substrates. Substrate preference is quercetin (flavonoid) = luteolin (flavonoid) > 5-hydroxyferulic acid (phenylpropanoid) >> apigenin (flavonoid) = kempferol (flavonoid) >> apigenin (flavonoid) = kempferol (flavonoid).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1992 (Rel. 23, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Caffeic acid 3-O-methyltransferase (EC 2 1.1.68) (S-adenosys]-Inmethionine:Caffeic acid 3-O-methyltransferase) (COMT) (CADMT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=cv. Apollo;
Gowri G., Bugos R.C., Campbell W.H., Maxwell C.A., Dixon R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 380; DB 1; Length 343;
; Pred. No. 2.4e-23;
68; Mismatches 131; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                   F43F2D306E18CB1C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       319 IINGKERKEEDWKKLFMEAGFOSYKI--SPFTGYL 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    365 AA
Biochem, Biophys. 351:243-249(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                SAM-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tch 20.1%; Score 380; al Similarity 30.4%; Pred. No. 2 102; Conservative 68; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                         Methyltransferase, Transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                               37821 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1992 (Rel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Medicago sativa (Alfalfa).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                               343 AA;
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                                                                                                                                 substrate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 MKWICHDWSDEHCLKRELKNCYEAL---PDNGKVIVAECILPVAPDSSLATKGVVHIDVIM 320
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         Molecular cloning
                                                                                                                 FUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid and of 5-hydroxyferulic acid to sinapic acid. The resulting products may subsequently be converted to the corresponding alcohols that are incorporated into lignins.

CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3.4-dihydroxy-transcinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-transcinnamate
                                                                                                                                                                                                                                                                                                                                      36 LKSALELDLLEIIAKAGPGAQISPIEIAS--QLPTINPDAPVMLDRMLRLLACYIILTCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 VRIHDNIEA---YALTAASELLVKSSE-LSLAPMVEYFLEPNCQGAWNQ----LKRWVHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 IVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 LKWMVELDIPDIIHSHSHGQPITFSELVSILQVPPTKTRQVQSLMRYLAHNGFFEI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BDLTV-----FEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVFEGLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the methyltransferase superfamily, Family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3D-structure
                                                          3-0-methyltransferase, a key enzyme of lignin biosynthesis.";
Plant Physiol. 97:7-14(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
"Stress responses in alfalfa (Medicago sativa L). X. Mand expression of S-adenosyl-L-methionine:caffeic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             se; Methyltransferase; 3
C14B0D75F979C6B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 LAHNPGGKERTQKEFEDLAKGAGFQGFKVHCNAFNTYI 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317 -ACIINGKERKEEDWKKLFMEAGFQSYKI--SPFTGYL 351
                                                                                    Plant Physiol. 97:7-14(1991).
-!- FUNCTION: Catalyzes the conversion of caffeic and of 5-hydroxyferulic acid to sinapic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 379.5; DB 1;
Pred. No. 2.9e-23;
63; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 VRTQQDGKVQRLYGLATVAKYLVKNEDGVSISAL-----
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(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR00051, SAM bind.
Pfam; PF00891, Methyltransf 2; 1
Lignin biosynthesis; Transferase,
SEQUENCE 365 AA, 39946 MW C14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDB; IKYW; 28-AUG-02.
PDB; IKYZ; 28-AUG-02.
InterPro; IRRO1601; Wethyltransf.
InterPro; IPRO1077; O_Metransf2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.1%;
31.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M63853; AAB46623.1; -.
PIR; T09673; T09673.
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       94 DNIEA------YALTAASELLVKSSE-LSLAPMVEYFLEPNCQGAWNQ----L 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---LMNODKVLM 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 KRWVHEEDLTV----FEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. Habanero;
Curry J., Mendoza M., O'Connell M.;
"Nucleotide sequence of a caffeic acid 3-0-methyltransferase gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid and of 5-hydroxyferulic acid to sinapic acid. The resulting products may subsequently be converted to the corresponding alcohols that are incorporated into lighins.

CATALYTIC ACTIVITY: 8-adenosyl-L-methionine + 3,4-dihydroxy-transcinnamate = 8-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-trans-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 LKMMVELDIPDIIHSHSHGQPITFSELVSILQVPPTKTRQVQSLMRYLAHNGFFEIVRIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Belongs to the methyltransferase superfamily. Family 2. COMT subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Capsicum chinense (Scotch bonnet) (Bonnet pepper).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamids; Solanales; Solanaceae; Capsicum.
NCBI_TaxID=80379;
                                                                                                                                                                                                                                                                                                                          15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Caffeic acid 3-O-methyltransferase (EC 2.1.1.68) (S-adenosysl-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.9%; Score 375.5; DB 1; Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                          Caffeic acid 3-0-methyltransferase (EC 2.1.1.68) (S-ad methionine:caffeic acid 3-0-methyltransferase) (COMT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       359 AA; 39636 MW; 4A836904EF6D7119 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001601; Methyltransf.
InterPro; IPR001077; O_Metransf2.
InterPro; IPR001051; SAM bind.
Ligan; PF00891; Methyltransf2; 1.
Lighin losynchesis; Transferase; Methyltransferase.
SEQUENCE 359 AA; 39636 MW; 4A836904EF6D7119 CRCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67; Mismatches 124;
                                                                                   319 IINGKERKEEDWKKLFMEAGFOSYKI--SPFTGYL 351
                                                                                                              300 NPGGKERTEKEFEALAKAAGPQGFQVFCNAFNTYI 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: Lignin biosynthesis.
SIMILARITY: Belongs to the me
                                                                                                                                                                                                                                                                                                        15-SEP-2003 (Rel. 42, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF081214; AAC78475.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.3%;
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                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 98; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                         RESULT 11
COMT CAPCH
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \stackrel{>}{\circ}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TV----FEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAFRDCNWVFEGLESIVD 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                260 VLHNWNDNDCMKILENCKBAISGBSKTGKVVVIDTVINENKDERQVTELKLLMDV-HMAC 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72
                                                                                                                                                                                                                                                                   MEDLINE=98181116; PubMed=9514654;
Gauthier A., Gulick P.J., Ibrahim R.K.;
"Characterization of two cDNA clones which encode O-methyltransferases for the methylation of both flavonoid and phenylpropanoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAUTION: It is not sure if OMT1 and OMT2 are really encoded by two different genes or if they represent cloning artifacts.
                                                                                                                                                                                                                                                                                                                                                                                       Arch. Biochem. Biophys. 351:243-249(1998).

-!- FUNCTION: Methylates CH residues of flavonoid and phenylpropanoid compounds and shows a higher affinity for flavonoid than phenylpropanoid substrates. Substrate preference is quercetin (flavonoid) = luteolin (flavonoid) = 5-hydroxyferulic acid (phenylpropanoid) > caffeic acid (phenylpropanoid) > apigenin (flavonoid) = kempferol (flavonoid).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 VLDGGIPPNKAYGMSSFEYHGTDPRPNKVPNKGMSDHSTITMKKVPQTYQGFQGLTSLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 VGGGTGATLTMILSKYPTIRCINFDLPHVIBDAPBYPGIEHVGGDMFVSVPKGDAIPMKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKWMVELDIPDIHSHSHGOPITFS--ELVSILQVP-PTKTRQVQSLMRYLA,HNGFFBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 VRIHDNIEAYALTAASELLVKSSE-LSLAPMYEYFLEPNCQGAWNQ----LKRWYHEEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVLLKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYIC ACTIVITY: S-adenosyl-L-methionine + 3,5,7,3',4'-
pentahydroxyflavone = S-adenosyl-L-homocysteine + 3-methoxy-
-!- PATHWAY: Phenylproyanoid pathway.
-!- PATHWAY: Phenylpropanoid pathway.
-!- MISCELLANEOUS: The Vmax value for flavonoid compounds is two to
threefold lower for OMT2 than for OMT1.
-!- SIMILARITY: Belongs to the methyltransferase superfamily. Family
                                                                      Chrysosplenium americanum (Golden saxifrage).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Saxifragales, Saxifragaceae; Chrysosplenium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34;
     (Flavonol 3-0-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 379; DB 1; Length 34; Pred. No. 2.9e-23; 68; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8D363A98330FDE4F CRC64;
  (EC 2.1.1.76)
                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAM-BINDING,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001601; Methyltransf.
InterPro; IPR001077; O Metransf2.
InterPro; IPR000051; SAM bind.
Pfam; PF00891; Methyltransf2.
Methyltransferase; Transferase.
Quercetin 3-0-methyltransferase 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       343 AA; 37868 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 20.1%;
Local Similarity 30.4%;
es 102; Conservative 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U16793; AAA86982.1;
                         methyltransferase
                                                                                                                                                                        NCBI_TaxID=36749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  substrate.
                                                                                                                                                                                                                                               TISSUE=Leaf
                                                                                                                                                                                                                                                                                                                                                                     compounds."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89 IVRIHD-NIE-AYALTAASELLVKSSE-LSLAPMVEYFLEPNCOGAWNO----LKRWVHE 141
FEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIP 250
                            KADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVTELKL 310
                                                                                                                  254 KADAIPMKWICHDWSDDHCIKLLKNCYEALPA---NGKVIIVECILPEAPDTSAATKSKV 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 LKWMVELDIPDIIHSHSHGQPITFSELVSILQVPPTKTR---QVQSLMRYLAHNGFFE-- 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 LKSAIELDLLELIKKSGAGAFVSPVDLAA--QLPTTNPDAHVMLDRILRLLTSYAILECR 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid and of 5-hydroxyferulic acid to sinapic acid. The resulting products may subsequently be converted to the corresponding alcohols that are incorporated into lignins.

CATALYTIC ACTILITY: S-adenosyl-L-methionine + 3.4-dihydroxy-transcinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-transcinnamate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PATHWAY: Lignin biosynthesis. SIMILARITY: Belongs to the methyltransferase superfamily. Family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CAOMT-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, lamiids, Lamiales, Lamiaceae, Nepetoideae, Ocimeae,
                                                                                                                                                                                                                                                                                                                                                                                                                                           2.1.1.68) (S-adenosysl-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Nucleotide sequences of two cDNAs encoding caffeic acid Omethyltransferases from sweet basil (Ocimum basilicum)."; (In) Plant Gene Register PGR99-105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CV. EXM-1;
Wang J., Dudareva N., Kish C.M., Simon J.E., Lewinsohn E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (COMT-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000051; SAM bind.
Pfam; PF00891; Methyltransf 2; 1.
Lignin blosynthesis; Transferase; Methyltransferase.
SEQUENCE 361 AA; 39528 MW; D6ABC3D6837AAC9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                methionine:caffeic acid 3-0-methyltransferase 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 371,5; DB 1
Pred. No. 1.3e-22;
                                                                                                                                                                            LMDVHM-ACIINGKERKEEDWKKLFMEAGFQSYK 343
                                                                                                                                                                                                                         311 HGDIIMLAHNPGGKERTEKDFEALANWGWFSRFR 344
                                                                                                                                                                                                                                                                                                                                                                       15-82P-2003 (Rel. 42, Created)
15-82P-2003 (Rel. 42, Last sequence update)
15-85P-2003 (Rel. 42, Last annotation update)
Caffeic acid 3-0-methyltransferase 1 (EC 2.1.
                                                                                                                                                                                                                                                                                                                                    361 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AF154917; AAD38189.1; -.
InterPro; IPR001601; Methyltransf.
InterPro; IPR001077; O_Metransf2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ocimum basilicum (Sweet basil)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97; Conservative
                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2. COMT subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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191
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                                                                                                                                                                                                                                                  257 LKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVTELKLLMDVHM 316
                                                                                                                                                                                                                                                                                               262 MKWICHDWSDEHCYKFLKNCYDAL---PQNGKVILARCVLPEAPDTGLATKNVVHIDVIM 318
142 EDLTV-----FEVSLGTPFWDFINKDPAYNKSFNEAMACDSCMLNLAFRDCNWVFEGLES 196
                                                                                                                                                                                                      202 VVDVGGGTGATLNMIVSKYPSIKGINFDLPHVIEDAPSYPGVEHVGGDMFVSVPKGDAIF 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tsai C.-J., Mielke M.R., Podila G.K., Chiang V.L.C.;
Submitted (JUL-1997) to the BMBL/GenBank/DBM databases.

-!- RUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid
and of 5-hydroxyferulic acid to sinapic acid. The resulting
products may subsequently be converted to the corresponding
alcohols that are incorporated into lignins.

-!- CATALYMIC ACTIVITY: 5-adenosyl-L-methionine + 3.4-dihydroxy-trans-
cinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-trans-
                                                                                                       42 SDAVVDGGIPFNKAYGMTAFEYHGTDPRFNKVFNQGMSNHSTITMKKILETYTGFDGLKT
                                                                                                                                                           197 IVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCIPKADAVL
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I, Malpighiales, Salicaceae, Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95288373; PubMed=7770534;
Tsai C.-J., Podila G.K., Chiang V.L.C.;
"Nuclectide sequence of a Populus tremuloides gene encoding
bispecific caffeic acid/5-hydroxyferulic acid O-methyltransferase.";
Plant Physiol. 107:1459-1459(1995).

    -!- TISSUB SPECIFICITY: Xylem.
    -!- PTM: The N-terminus is blocked.
    -!- SIMILARITY: Belongs to the methyltransferase superfamily. Family

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bugos R.C., Chiang V.L.C., Campbell W.H.; "CDNA cloning, sequence analysis and seasonal expression of lignin-bispecific caffeic acid/5-hydroxyferulic acid 0-methyltransferase o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Catteic acid 3-0-methyltransferase 1 (BC 2.1.1.68) (S-adenosysl-L-methionine:caffeic acid 3-0-methyltransferase 1) (COMT-1) (CAOMT-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 165-184; 335-346 AND 349-359.
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                                                                                                                                                                                                                                                                                                                                              317 -ACIINGKERKEEDWKKLFMEAGFQSY 342
                                                                                                                                                                                                                                                                                                                                                                                        319 LAHNPGGKERTEKEFQGLAKAAGFKQF 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant Mol. Biol. 17:1203-1215(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Populus tremuloides (Quaking aspen)
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SEQUENCE FROM N.A.
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       (See http://www.isb-sib.ch/announce/
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"Molecular cloning and tissue-specific expression of two genes that
encode caffeic acid O-methyltransferases from Populus kitakamiensis.";
Plant Sci. 113:157-165[1996].
-!- FUNCTION: Catalyzes the conversion of caffeic acid to ferulic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 SLKDLPDGKVERL-----YGLAPVCKFLTKNEDGVSVSPLCLMNQDKVLMESWYYLKDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDERQVTELKLLMDVHM-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 WICHDWSDAHCLKFLKNCYDAL---PENGKVILVECILPVAPDTSLATKGVVHVDVIMLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKTAIBLDLLBIMAKAGPGAFLSTSEIASHL---PTKNPDAPVWLDRILRLÄASYSILTC
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I, Malpighiales, Salicaceae, Populus.
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15-SEP-2003 (Rel. 42, Last annotation update)
Caffeic acid 3-O-methyltransferase 1 (EC 2.1.1.68) (S-adenosysl-L-methylorine:caffeic acid 3-O-methyltransferase 1) (COMT-1) (CAOMT-1)
                                                                                                                                                                                                                                                                                                                                                                                           29;
                                                                                                                                                                                                                                                                                                                                         DB 1; Length
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                                                                                            EMEL, U13171; AAB61731.1; -
EMEL, U13171; AAB61731.1; -
PIR, S18568; S18568.
InterPro; IPR001601; Methyltransf.
InterPro; IPR000051; SAM bind.
Pfam; PF00891; Methyltransf. 2; 1.
Lignin biosynthesis; Transferase; Methyltransferase.
SEQUENCE 365 AA; 39805 MW; A6CECDEA4E0007CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        69; Mismatches 132;
                                                                                                                                                                                                                                                                                                                         19.7%; Score 371.5; DB 1
20.7%; Pred. No. 1.3e-22;
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entities requires a license agreement (or send an email to license@isb-sib.ch)
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SEQUENCE FROM N.A.
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CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3.4-dihydroxy-transcinnamate = S-adenosyl-L-homocysteine + 3-methoxy-4-hydroxy-transcinnamate
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids 1; Rosales; Rosaceae; Amygdaloideae; Prunus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (S-adenosysl-L-
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from Prunus amygdalus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 365;
                                                                                                                                                                                                                                                                                      InterPro; IPR000051; SAM bind.
Pfam; PF000891; Methyltransf 2; 1.
Lignin biosynthesis; Transferase; Methyltransferase.
SRQUENCE 365 AA; 39791 MW; D6005B10FE55B83C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                              19.5%; Score 368.5; DB 1; 29.7%; Pred. No. 2.2e-22; iive 68; Mismatches 133;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Caffeic acid 3-O-methyltransferase (EC 2.1.1.68)
methionine:caffeic acid 3-O-methyltransferase) (C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ä.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=cv. Texas; TISSUE=Root;
Garcia-Mas J., Messeguer R., Arus P.,
"The caffeic acid O-methyltransferase
(In) Plant Gene Register PGR95-006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HNPGGKERTEKEFEGLANGAGFOGFEV
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InterPro; IPR001077; O_Metransf2.
                                                                                                                                                                                                                  EMBL; D49710; BAA08558.1;
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97; Conserv
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.5%; Score 367.5; DB 1; Length 365;
30.7%; Pred. No. 2.7e-22;
ive 65; Mismatches 133; Indels 37; Gaps 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 FMKWICHDWSDEHCLKFLKNCYAAL---PDNGKVILGECILPVAPDSSLATKGVVHIDVI 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 EIVRIHD-NIE-AYALTAASELLVKSSE-LSLAPMVEYFLEPNCQGAWNQ----LKRWVH 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 SIRTLADGKVERLYGLGPVCKFLTKNEEGVSIAPL------C--LMNQDKVLLBSWYH 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 LKWMVELDIPDIIHSHSHGQPIIFSELVSILQVPPIKIR----QVQSLMRYLAHNGF--F 87
                        PATHWAY: Lignin biosynthesis.
SIMILARITY: Belongs to the methyltransferase superfamily. Family
2. COMT subfamily.
                                                                                                                                                                                                                                                                                                                         InterPro; IPR001601; Methyltransf.
InterPro; IPR001077; O_Metransf2.
InterPro; IPR001077; O_Metransf2.
InterPro; IPR001051; SAM bind.
Pfam; PF00891; Methyltransf2; 1.
Lignin biosynthesis; Transferase; Methyltransferase.
SEQUENCE 365 AA; 39762 MW; C8C4BFEETR018087 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           316 M-ACIINGKERKEEDWKKLFMEAGFOSYKI--SPFTGYL 351
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Best Local Similarity 30.7%
Matches 104; Conservative
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1 MASSLNNGRKASEIFQGQAL......PQSYKISPFIGYLSLIEIYP 358
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ALIGNMENTS

	4.	60	120
T 1 9 9022309; PRELIMINARY; PRT; 352 AA. 0022309; 01-JAN-1998 (TrEMBLrel. 05, Created) 01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 7-Comethyltransferase. 7-Comethyltransferase. 7-Comethyltransferase. 7-Comethyltransferase. 7-Comethyltransferase. 7-Comethyltransferase. 7-Comethyltransferase. 7-Comethyltransferase. 7-Comethyltransferase. 8-Comethyltransferase. 8-Comethyltransf	Score 1295; DB 10; Length 352; Pred. No. 9.5e-102; 55; Mismatches 53; Indels 6; Gaps	MASSLINNGRKASBIFOGOALLYKHLIGFIDSKCLKWMVELDIPDIIHSHSHGOPITFSEL 	OVPPTKTROVOSIMRYLAHNGFFEIVRIHDNIBAYALTAASELLVKSSELSLAPMV
T. 1 022309 PRELIMINARY; PRT 022309; 01.JAN-1998 (TEBMELRE1. 05, Creat 01.JAN-2002 (TEBMELRE1. 20, Last 01.JAN-2002 (TEBMELRE1. 20, Last 01.JAN-2002 (TEBMELRE1. 20, Last 01.JAN-2002 (TEBMELRE1. 20, Last 01.JAN-2003 (AIR) Medicago sativa (AIfalfa). Eukaryota; Viridiplantae; Strepto Spermatophyta; Magnoliophyta; eud eurosids I. Fabales; Fabaceae; Pa NCBI TaxID=3879; NCBI TaxID=3879; SEQUENCE FROM N.A. MEDLINE=98145455; PubMed=9484461; He X.Z., Reddy J.T., Dixon R.A.; "Stress responses in alfalfa (Med methyltransferase."; FROMO107; AAC49927.1; InterPro; IPRO0107; Methyltransf Plant Mol. Biol. 36:43-54 (1998). EMBL; AF000976; AAC49927.1; InterPro; IPRO01071; Omethyltransf Plant Pro; IPRO01071; Omethyltransf Plant Pro; IPRO01071; Omethyltransf Plant Pro; IPRO01071; Omethyltransf2: InterPro; IPRO01071; Omethyltransf2:	Similarity 68.2%; 14; Conservative	SSLNNGRKASEIFQGQ : : SSI-NGRKPSEIFKAQ	ilovpptktrovoslmi :
RESULT 1 022309 AC 022309; TO 01-7AN-1998 (TEMBLED) TO 1-7AN-1998 (TEMBLED) TO	Query Match Best Local Simi Matches 244;	1 MAS MAS	61 VSI
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176 NLALRDCDFVFDGLESIVDVGGGTGTTAKIICETFPKLKCIVFDRPQVVENLSGSNNLTY 235
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296 DENQVTQIKLIMDVNMAC-INGKERNBEBWKKLFIBAGPQHYKISPLIGFLSLIEIXP 352
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae, Medicago.
                                                                                                                                                                                                                                                                                                                                                             MEDLINE-9814545; PubMed-9484461; He X.Z., Reddy JT., Dixon R.A.; Stress responses in alfa (Medicago sativa L). XXII. CDNA cloning and characterization of an elicitor-inducible isoflavone 7-0-
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Last annotation update)
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01-JAN-1998 (TrEMBLrel. 05, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
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InterPro; IPR01077; O Metransf2.
Pfam; PF00891; Methyltransf 2; 1.
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EMBL; U97125; AAC49928.1; -.
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       58 VSILQVPSSKIGNVRRLMRYLAHNGFFEIITKEE--ESYALTVASELLVRGSDLCLAPMV 115
                                             EYFLEPNCOGAWNOLKRWVHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQML 180
                                                                    181 NLAFRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTF 240
                                                                                                                                         176 NLALRDCDFVFDGLESIVDVGGGTGTTAKIICETFPKLKCIVFDRPQVVBNLSGSNNLTY 235
                                                                                                                                                                                            241 VGGDMFKCIPKADAVLLKLVLHNWNDNDCMKILBNCKBAISGESKTGKVVVIDTVINENK 300
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                                                                                                                                                                                                                                                                    DERQVIELKLIMDVHMACIINGKERKEEDWKKLFMEAGFQSYKISPFIGYLSLIEIYP 358
                                                                                                                                                                                                                                                                                        296 DENOVTOIXLLMDVNMAC-LNGKERNEEBWKKLFIEAGFOHYKISPLTGFLSLIEITY 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MASSI-NGRKPSEIFKAQALLYKHIYAFIDSMSLKWAVEMNIPNII--QNHGKPISLSNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae, Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       He X.Z., Reddy J.T., Dixon R.A.; "Stress responses in alfalfa (Medicago sativa L). XXII. cDNA cloning and characterization of an elicitor-inducible isoflavone 7-0-methyltransferase.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31B95226966C1C98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                352 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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InterPro; IPR001601; Methyltransf.
InterPro; IPR001077; O Metransf2.
Pfam; PF00891; Methyltransf2; 1.
Methyltransferase; Transferase.
SEQUENCE 352 AA; 39604 MW; 31B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98145455; PubMed=9484461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant Mol. Biol. 36:43-54(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Medicago sativa (Alfalfa).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 243; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7-0-methyltransferase.
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46.0%; Score 867.5; DB 48.7%; Pred. No. 2e-65;
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01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Orcinol O-methyltransferase.
                                                                                        Conservative
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                                    Query Match
Best Local Similarity
Matches 174; Conserv
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Q8L5K8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           He X.Z., Dixon R.A.;
"A cDMA of an additional member of the isoflavone-O-methyltransferase (IOMT) of the family in Medicago sativa (Accession No. AF023481)
(PGR97-170).";
Plant Physiol. 115:1289-1289(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLAFRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTF
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Pisuva yviridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                                                                                                                                                                                                       DB 10; Length 343;
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                                                                                                                                                                                                                                                                                                                                                  343 AA; 38433 MW; 296665211415C7BB CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                 Score 1237.5; DB 10;
Pred. No. 7e-97;
....rhes 50;
                                                                                                                                                                                                                                                                                                                                                                                   65.6%; Scc...
66.8%; Pred. No. /e...
'ive 55; Mismatches
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                                                                                                                                                                                                                                      EMBL, AP023481; AAB88294.1; -- interPro; IPR001077; O Metransf2. Pfam; PF00891; Methyltransf_2; 1. Transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 238; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                SEQUENCE FROM N.A.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.
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X MEDLINE=2105322;

X MEDLINE=2105322;

A Lavid N., Wang J., Shalit M., Guterman I., Bar E., Beuerle T.,

A Menda N., Shafir S., Zamir D., Adam Z., Vainstein A., Weiss D.,

A Pichersky E., Lewinschn E.;

A Pichersky E., Lewinschn E.;

T Comethyltransferases involved in the biosynthesis of volatile

I phenolic derivatives in rose petals.";

Plant Physiol. 129-1899-1907(2002).

I Phanolic derivatives in rose petals.";

R EMBL, ARSO2433; AAM23004.1; --.

R InterPro; IPR001601; Methyltransf.

InterPro; IPR001601; Methyltransf.

I Transferase; Methyltransf 2; 1.

Transferase; Methyltransferase.
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46.2%; Pred. No. 5e-65;
tive 68; Mismatches 119; Indels
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Last sequence update)
Last annotation update)
DB 10;
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Plant Physiol. 129:1899-1907(2002).
EMBL, AF502434, AAM23005.1;
EMBL, AF5004010, Methyltransf.
InterPro; IPR001601; Methyltransf2.
InterPro; IPR001601; SAM.bind.
Ffan; PP00891; Methyltransf2.
Transferase; Methyltransferase.
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MEDLINE=22167322; PubMed=12177504;
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                                                                         01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23, Orcinol O-methyltransferase.
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01-MAR-2003
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            EPNCQGAWNQLKRWVHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQML-NLA
                                                                                         DMFEAVPPADTVILKWILHDWSDEECIKILERSRVAITGKEKKGKVIIIDMMENOKGDE
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STRAIN=CV. Old Blush;
Cock J.Mark, Scalliet G., Hugueney P.;
"Characterisation of a novel O-methyltransferase involved in the biosynthesis of 3,5-dimethoxytoluene and 1,3,5-trimethoxybenzene, "major scent components of rose flowers.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ439741. CAD29458.1; -.
Transferase; Methyltransferase.
Transferase; Methyltransferase.
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46.2%; Pred. No. 5e-65;
live 68; Mismatches 119; Indels
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(TrEMBLrel. 23, Last sequence update)
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Eukaryota, Viridiphantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I, Rosales, Rosaceae, Rosoideae, Rosa.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Lavid N., Wang J., Shalit M., Guterman I., Bar E., Beuerle T., Menda N., Shafit S., Zamir D., Adam Z., Vainstein A., Weiss D., Pichersky B., Lewinschn E., "O-methyltransferases involved in the biosynthesis of volatile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 366;
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Last annotation update)
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                                                           RKASEIFQGQALLYKHLLGFIDSKCLKWWVELDIPDIIHSHSHGQPITFSELVSILQVPP
                                                                                                                   RASHELLQAQAHIWNHIFSFINSLSLKCAVQLDIPDVI--QKHGQPMTLSELVSALPISP
                                                                                                                                                                                                                                                                                                 CQGAWNQLKRWVHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQML-NLAFRD
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosid
eurosids I, Rosales, Rosaceae, Rosoideae, Rosa.
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      4,
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   66; Mismatches 123; Indels
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AJ439744; CAD29556.1; -.
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Last annotation update)
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   159; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 DPVLTTPWNYLSTWFQNEDPTPFDTAHGMTFWDYGNHQPSIAHLFNDAMASDARLVTSVI 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 IDDCKGVFEGLESLVDVGGGTGTVAKAIADAFPHIECTVLDLPHVVADLQGSKNLKYTGG
                                                                                                         STRAIN-CV. Old Blush,
Cock J.Mark, Scalliet G., Hugueney P.;
Cock J.Mark, Scalliet G., Hugueney P.;
Charterisation of a novel O-methyltransferase involved in the biosynthesis of 3.5-dimethoxytoluene and 1,3,5-trimethoxybenzene, two major scent components of rose flowers.";
Submitted (WAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ439742; CAD29459.1;
Transferase, Methyltransferase.
SEQUENCE 366 AA; 41226 MW; CAF4B17D3230D29E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 NNGRKASEIFQGQALLYKHLLGFIDSKCLKWMVELDIPDIIHSHSHGQPITFSELVSILQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGG
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I; Rosales, Rosaceae, Amygdaloideae, Prunus.
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Mbeguie-A-Mbeguie D., Gomez R.-M., Fils-Lycaon B.;
"Sequence of an O-Methyltransferase from Apricot Fruit (Accession No. 982011). Gene Expression During Fruit Ripening (PGR97-118).";
Plant Physiol. 114:1569-1569(1997).
EMBL; U82011; AAB71213.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                  44.9%; Score 847.5; DB 10; Length 366; 45.6%; Pred. No. 1e-63;
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Last annotation update)
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Pred. No. 7.7e-63;
eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.
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InterPro; IPR001077; O Metransf2.
InterPro; IPR000051; SAM bind.
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01-JAN-1998 (TrEMBLrel. 05,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                       SEQUENCE FROM N.A
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                            NCBI_TaxID=74649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       312
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RESULT 12 Q8GU22

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61 PIHPKKSNCVYRLMRILVHSGFFCRQKLSELDEBEGYVLTDASRLLLKDDPLSARPFLLG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 QVPPTKTRQVQSLMRYLAHNGFFBIVRIH--DNIBAYALTAASBLLVKSSBLSLAPMVBY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 GGDMFKCIPKADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKD 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CV. EMX-1; TISSUB=Peltate glandular trichome;
Gang D.R., Lavid N., Zubieta C., Chen F., Beuerle T., Lewinsohn E.,
Noel J.P., Pichersky E.;
"Characterization of Phenylpropene O-Methyltransferases from Sweet
Basil: Facile Change of Substrate Specificity and Convergent Evolution
within a Plant OMT Pamily.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 DOSI-ETQLFFDMLMMVLFTGKERTEKEWAKLFSDAGFSDYKITPICGLRYLLEVYP 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 BRQVTELKLIMDVHMACIINGKERKEEDWKKLFMEAGFQSYKISPFTGYLSLIEIYP 358
                                                           Prunos dulcis (Almond) (Prunus amygdalus).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots, Rosidae,
eurosids I; Rosales, Rosaceae, Amygdaloideae, Prunus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLEPNCQGAWNQLKRWVHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAFRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Asteridae, lamiids, Lamiales, Lamiaceae, Nepetoideae, Ocimeae, Ocimum.
NCBI_TaxID=39350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 LNNGRKASEIFQGQALLYKHLLGFIDSKCLKWMVELDIPDIIHSHSHGQPITFSELVSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-methyltransferase.
0cimum basilicum (sweet basil).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                   Suelves M., Puigdomenech P.; "Specific mRNA accumulation of a gene coding for an O-methyltransferase in almond (Prunus amygdalus, Batsch) flower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.3%; Pred. No. 4.0e-00, cive 70; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 4CC6F169513F4EA9 CRC64;
                        Last annotation update)
      Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 757; DB 10;
Pred. No. 4.8e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               357 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.1%; Score 757;
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                                                                                                                                                                                                                                                                                                                               EMBL, AJ223151; CAA11131.1, -.
InterPro; IPR001601; Methyltransf.
InterPro; IPR001077; O Metransf2.
Fam; PF00891; Methyltransf2; 1.
Methyltransferase; Transferase.
SEQUENCE 356 AA; 40206 MW; 4CC
  07,
                                                                                                                                                                                                                                                                                                                      Plant Sci. 134:79-88(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
  01-AUG-1998 (TrEMBLrel. 01-MAR-2002 (TrEMBLrel. O-methyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                               STRAIN=cv. Texas;
                                                                                                                                                    NCBI_TaxID=3755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123
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Q93WU2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRDCNWVFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 VIIDDCKGVFEGLESLYDVGGGTGTVAKAIADAFPHIECTVLDLPHVVGDLQGSKNLKYT 240
                                                                              GGDMFEAVPPADTVLLKWILHDWNDEECIKILKRSRVAITSKDKKGKVIIIDMMMENQKG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VPPTKTROVOSLMRYLAHNGFFEIVRI-HDNIEAYALTAASELLVKSSELSLAPMVEYFL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 DPVLTNPWNYLSTWFQNDDPTPFDTAHGMTFWDYGNHQPSIAHLFNDAMASDARLVTSVI 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DMFKCIPKADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKDER 303
                                           GGDMFKCIPKADAVLLKLVLHNWNDNDCMKILENCKEAISGESKTGKVVVIDTVINENKD 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHGEHSNELLHAQAHIWNHIFSFINSMSLKSAIQLGIPDII--NKYGYPMTLSELTSALP 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 NNGRKASEIFQGQALLYKHLLGFIDSKCLKWMVELDIPDIIHSHSHGQPITFSELVSILQ
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN=cv. Lady Hillington;

STRAIN=cv. Lady Hillington;

STRAIN=cv. Lady Hillington;

STRAIN=cv. Lady Hillington;

Cock J.Mark, Scalliet G., Hugueney P.;

Characterisation of a novel 0-methyltransferase involved in the biosynthesis of 3,5-dimethoxytoluene and 1,3,5-trimethoxybenzene, biosynthesis of 3,5-dimethoxytoluene and 1,3,5-trimethoxybenzene, major scent components of rose flowers.";

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ439743; CAD29555.1;

Transferase; Methyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4,
                                                                                                                          302 ERQVTELKLLMDVHMACIINGKERKEEDWKKLFMEAGFQSYKISPFTG 349
                                                                                                                                                  Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 QVTELKLIMDVHMACIINGKERKEEDWKKLFMEAGFQSYKISPFTG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.3%; Score 817; DB 10; Length 3
45.1%; Pred. No. 3.8e-61;
tive 67; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          348 348
348 AA; 39034 MW; OAFD4D325AODBBID CRC64;
                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 23, Created) (TrEMBLrel. 23, Last sequence update) (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I; Rosales; Rosaceae; Rosoideae; Rosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.
                                                                                                                                                                                                                                                                             348 AA
                                                                                                                                                                                                                                                                                                                                                                               Orcinol O-methyltransferase (Fragment).
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                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                       Rosa hybrid cultivar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=128735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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01-MAR-2003
                                                                                                                                                                                                                                                                                                                  01-MAR-2003
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                                           242
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                                                                                                                                                                                                                                                  131
                                                                                                                                                                                                                                                                     CFORLMRALVNSNFFIEENNSNNQEVCYWLTPASCLLIKEAPLTVTFLVQVVLDPTFTNP 131
                                                                                                                                                                                                                                                                                                           WNQLKRW-VHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLNLAF-RDCNW 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69
                                                                                                                                                                                                                                                                                                                                       WHHMSEWFTHEKHATQFEAANGCTFWEKLANEPSKGRFFDEAMSCDSRLIAHVFTKDYKH 191
                                                                                                                                                                                          72
                                                                                                                                                                                                                    71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O-methyltransferase.
Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Gentianales; Apocynaceae; Rauvolfioideae; Vinceae;
Catharanthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 KASEIFQGQALLYKHLLGFIDSKCLKMWVELDIPDIIHSHSHGQPITFSELVSILQVPPT
                                                                                                                                                                                                           13 EIFQGQALLYKHLLGFIDSKCLKWMVELDIPDIIHSHSHGQPITFSELVSILQVPPTKTR
                                                                                                                                                                                                                                                    73 QVQSLMRYLAHNGFFEIVRIHDNIE-AYALTAASELLVKSSELSLAPMVEYFLEPNCQGA
                                                                                                                                                                                                                                                                                                                                                                       VFEGLESIVDVGGGTGITAKIICEAFPKLKCMVLERPNVVENLSGSNNLTFVGGDMFKCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schroeder J.; "A flavonol O-methyltransferase from Catharanthus roseus performing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.5%; Score 726.5; DB 10; Length 347; 41.7%; Pred. No. 1.8e-53; cive 73; Mismatches 117; Indels 17;
                                                                                                                                                            ..
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                                                                                                                             38.9%; Score 734; DB 10; Length 357; 41.5%; Pred. No. 4.4e-54; ive 75; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cacace S., Schroeder G., Wehinger E., Strack D., Schmid J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38789 MW; 7FB24AC0BC97AB35 CRC64;
                                                                                                   40236 MW; FC050C48BF6D719C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22371605; PubMed=12482447;
                        InterPro; IPR001601; Methyltransf.
InterPro; IPR00107; O'Merransf2.
InterPro; IPR000051; SAM bind.
Pfam; PF00891; Methyltransf2; 1.
Methyltransferase, Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     two sequential methylations.";
Phytochemistry 62:127-137(2003).
EMBL; AX127569; AAM97498.1;
Transferaes, Methyltransferaes.
SEQUENCE 347 AA; 38789 MW; 71
                                                                                                                                              larity 41.5%; Proceed To.
             EMBL; AF435008; AAL30424.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 41.7°
Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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SEQUENCE FROM N.A.
                                                                                                     357 AA;
                                                                                                                                             Local Similarity
hes 145; Conserv
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Matches
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70 KTRQVQSLMRYLAHNGFFEIVRIHDNIEAYALTAASELLVKSSELSLAPMVEYFLEPN-- 127

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Db 62 KAPYTHRIMRILVAAGYES----EEPRAVYSTTSLSRILVKNOPLNLR---EFVLSANEI 114

QY 128 --CQGAMNQLKRWVHEEDLTVFEVSLGTPFWDFINKDPAYNKSFNEAMACDSQMLN-LAF 184

Db 115 AEVG-WNALSEWFONDATAFQTAGTTYWEYLSQD-KYGKTFDQLMATDSLISKLLI 172

QY 185 RDCNWVPEGLESIVDVATAFQTAGTTYWEXLSQD-KYGKTFDQLMATDSLISKLLI 172

Db 173 PDYNXLPEGLISLVOVGGGTGTTAKICCAFFEKKGWVLERPWVVNLSGSNNLTFVGGD 244

Db 173 PDYNXLPEGLISLVOVGGGTGTLAGAVAKAFPNLKCTVFEQPHVIADLEAKGNLEFVGGD 232

QY 245 MFKCIPKADAVLLKTVLHNWNDCMKILENCKEAISGESKTGKVVVLDTVI-NENKDER 303

QY 245 MFKCIPKADAVLLKSVLHDWKDEDSVKILKNCKKAIPEKEKGKVIVIDIVLMDSKKHDN 292

QY 245 WFKCIPKALMDVHMACIINGKERKEEDWKKLFMEAGFOSYKISPFTGYLSLIEIYP 358

DD 233 MFEKIPSANAILLKSVLHDWKDEDSVKILKNCKKAIPEKEKGKVIVIDIVLMDSKKHDN 292

QY 304 QVTELKLLMDVHMACIINGKERKEEDWKKLFMEAGFOSYKIFPMLDFRSPIEUYP 347

Search completed: November 10, 2003, 03:21:16
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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ALIGNMENTS

	mRNA linear PLN 04-MAR-2003	ethionine:						a; Tracheophyta;	eudicots;	sae; Galegeae;		
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	1121 bp	Glycyrrhiza echinata D70MT mRNA for S-adenosyl-L-methionine:	י בייים ביז דרו שזופים ומפם '	AB091685.1 GI:28804593		echinata	echinata	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Galegeae,		
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RESULT 1 AB091685	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM					REFERENCE

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1 (bases 1 to 1284)
He,X.Z., Reddy,J.T. and Dixon,R.A.
Stress responses in alfalfa (Medicago sativa L). XXII. cDNA cloning and characterization of an elicitor-inducible isoflavone
7-O-methyltransferase
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He,X.Z., Reddy,J.T., Guo,J.Z. and Dixon,R.A.
Direct Submission
Submitted (32.APR-1997) Plant Biology Divsion, The
Noble Foundation, 2510 Sam Noble Parkway, Ardmore,
Location/Qualifiers
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                                                                                                                                                                                                                                       Submitted (14-SEP-2002) Shin-ichi Ayabe, Nihon University, Department of Applied Biological Sciences; Kameino 1866, Fujisawa, Kanagawa 25-9510, Japan (E-mail:ayabe@brs.nihon-u.ac.jp, Tel:81-466-84-3703, Fax:81-466-80-1141)
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                 cDNA cloning and biochemical characterization of s-adenosyl-L-methionine: 2,7,4'-trihydroxyisoflavanone 4'-o-methyltransferase, a critical enzyme of the legume isoflavonoid phytoalexin pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="cloning vector: lambda ZapII~cultured
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product="S-adenosyl-L-methionine: daidzein
                                                                                                           Plant Cell Physiol. 44 (2), 103-112 (2003)
22497945
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/mol_type="mRNA"
/db_xref="taxon:46348"
/cell_line="Ak-1"
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Akashi,T., Aoki,T. and Ayabe,S.
Direct Submission
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48. .1121
/gene="D7OMT"
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0; Mismatches 251;
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Dixon,R.A. and He,X.Z.
Isoflavonoid methylation enzyme
Patent: WO 0011736-A 1 30-NOV-2000,
The Samuel Roberts Noble Foundation,
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lonhgxristsnuy-axsindypsskidnyrrelmyrrebeityresperativasel
lonhgxristsnuy-axsindypsskidnyrrelmyrrebeityresperativasel
longsbiclapnyrocyldpriscopyrfoglesivdyggggfgtgtyrigscepyperciye
byspoyyeniscssnuktyvggdyffsiphadayllkyriehnwydydcirilkkckevyr
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Pred. No. 1.1e-136;
); Mismatches 250;
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                   type="mRNA"
xref="taxon:3879"
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Medicago sativa Medicago sativa

DEFINITION ACCESSION VERSION KEYWORDS SOURCE

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1 (Lases 1 to 1231)
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1 (Lases 1 to 1231)
2 He,X.Z., Reddy,J.T. and Dixon,R.A.
2 Stress responses in alfalfa (Medicago sativa L). XXII. cDNA cloning and characterization of an elicitor-inducible isoflavone
7-O-methyltransferase
1 Plant Mol. Biol. 36 (1), 43-54 (1998)
2 P44451
2 P84451
2 (Bases 1 to 1231)
2 (Bases 1 to 1231)
3 He,X., Reddy,J.T. and Dixon,R.A.
5 Libract Submission
1 Submitted (11-APR-1997) Plant Biology Division, The Samuel Roberts
Noble Foundation Inc., 2510 Sam Noble Parkway, Ardmore, OK 73401, USA
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/product="isoflavone-0-methytransferase"
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/note="7-IOMT; 7-0-methyltransferase"
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Pred. No. 2.6e-136;
0; Mismatches 251;
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/codon_start=1
/poduct=7-0-methyltransferase"
/protein_id="Aq449927_1"
/db_xref="d1:2580584"
/tb_xref="d1:2580584"
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LVRGSDLCLAPMVECVLDPFLSGSYHELKKWIYEEDLTLFGVTLGSGFWDFLDKNPEY
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DRPQVVENLSGSNNLTYVGGDMFTSIPNADAVLLKYILHNWTDKDCLRILKKCKRAVT
NDGKRGKVTIIDMVINEKKDENQVTQIKLLMDVNMACLNGKERNEEEWKKLFIEAGFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACATTIGCTTGGCTTCATAGATTCTAAGTGTCTAAAATGGATGGTTGACCTTGACATAC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCGACATAATCCACAGCCATAGCCATGGCCAACCCATTACTTTTTCAGAGTTGGTGTCAA 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACACATATATGCCTTCATAGATTCCATGTCTTTAAATGGGCTGTTGGAATGAACATAC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGCTTCAGAGTTACTTGTCAAAAGCAGTGAGCTTAGTTTAGCTCCAATGGTTGAGTATT
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X
Foundation, 2510 Sam Noble Parkway, Ardmore,
Location/Qualifiers
1. 1227
/organism="Medicago sativa"
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Pred. No. 1.4e-135;
0; Mismatches 253;
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                                                                                        /mol_type="mRNA"
/db_xref="taxon:3879"
1. _1227
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182 c 237 g
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24. .1082
/gene="7-IOMT(9)"
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Best Local Similarity 75.8%;
Matches 839; Conservative
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He,X.Z., Reday,J.T. and Dixon,R.A.
Stress responses in alfalfa (Medicago sativa L). XXII. cDNA cloning and characterization of an elicitor-inducible isoflavone
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Bark.Z., Reddy,J.T., Guo,J.Z. and Dixon,R.A.

Dixect Submission

Submitted (23-APR-1997) Plant Biology Divsion, The Samuel Roberts
                                                                                                                                                                                                                                                                                                                                                                                                                            GGGACATGITCACATCTATTCCTAATGCTGATGCAGTTTTGCTTAAGTATATTCTACATA
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ATCTTACACTCTTTGGTGTTACTTTAGGATCTGGTTTTTTGGGATTTTCTTGATAAAATC
                                             CTGCATATAACAAGTCATTCAATGAGGCAATGGCTTGTGATTCTCAGATGTTGAACTTGG
                                                                              CIGAATATAATACCICATITAATGATGCAATGCTAGTGATTCTAAATTGATAAACTTGG
                                                                                                                                CGTTTAGAGATTGCAATTGGGTCTTTGAGGGACTGGAATCCATTGTGGATGTTGGTGGTGT
                                                                                                                                                                         CATTGAGAGATTGTGTTTTGATTGATTGGAATCAATTGTGGATGTTGGTGGTG
                                                                                                                                                                                                                                                          GAACTIGGAACAACTIGCTAAGATTATTTGTGAGACTTTTCCTAAGTTGAAATGTATTGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>ATTGGACTGATAAGGATTGCCTAAGGATACTGAAGAATGTAAAGAAGCTGTTACAAATG</u>
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Medicago sativa 7-0-methyltransferase
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AF000976.1 GI:2580583
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Plant Mol. Biol. 36 (1
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DIPRQVVENLSGSNNLTYVGGDNFTSIPNADAVLLKDCLRILKKCKERATNDGFRGKVT
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IQNHGKPISLSNLVSILQVPSSKIGNVRRLMRYLAHNGFFEIITKEEESYALTVASEL
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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Medicago.
1 (bases 1 to 1194)
He,X.Z. and Dixon,R.A.
A cDNA of an additional member of the
isoflavone-0-methyltransferase (IOMT2) gene family in Medicago
Sativa (Accession No. AF023481) (PGR97-170)
Plant Physiol. 115, 1289 (1997)
2 (bases 1 to 1194)
He,X.Z. and Dixon,R.A.
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                                                                                    GGGACATGTTCACTATTCCTAATGCTGATGCAGTTTTGCTTAAGTATATTCTACATA
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                                                      GGGACATGTTTAAATGCATCCCCAAGGCTGATGCAGTTCTGCTTAAGTTGGTTTTACATA
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Submitted (09-SEP-1997) Plant Biology Divsion, The
Noble Foundation, 2510 Sam Noble Parkway, Ardmore,
Location/Qualifiers
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/function="methylates 7-hydroxyl-group
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'product="o-methytransferase"
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/organism="Medicago sativa"
/mol_type="mRNA"
/db_xref="taxon:3879"
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/db_xref="GI:2565273"
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400 418 460 475 520 589

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299 GAAGCATATGCTCTCACTGCTTCAGAGTTACTTGTCAAAAGCAGTGAGCTTAGTTTA 358
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                                                                       AACAATGGCCGTAAAGCAAGTGAGATTTTTCAAGGTCAAGCTCTCTTGTACAAACATTTG
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Mismatches 399;
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IHNHGKPITLPBLASALKLHPSKVGILYRFLRLLTHNGFFAKTTVPSQNGKDGBEBEB
TAYALTPPSKLLVKGKPTASTVRGALHPSSLDWMRSSEKWFKEDKELTLFRSATGB
FWDFLNKDSEGGTLSMPQEAMAADSOMPKLALKECRHVFBGIBSLYDVGGGTGGTY
LIHEBFPHLKGTVYPOPQVVGNLSGNENLKFVGGDMFKSIPPADAVLLKWYLHDWNDE
LSLKILKNSKBAISGKOKEGKYIIDISIDEAGGDRELTELQLDYDLVKWYLHDWNDE
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Glycyrthiza echinata
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Fracheophyta,
Spermatophyta, Magnoliophyta, endicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae; Papilionoideae, Galegeae,
Glycyrrhiza.
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Assah.T. Aoki.T. and Ayabe,S.

Direct Submission
Submitted (14-SEP-2002) Shin-ichi Ayabe, Nihon University,
Department of Applied Biological Sciences; Kameino 1866, Fujisawa,
Kanagawa 252-8510, Japan (B-mail:ayabe@brs.nihon-u.ac.jp,
Tel:81-466-84-3703, Pax.81-466-80-1141)
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AAGAGAGAAAAAGAAGATTGGAAGAAACTCTTCATGGAAGCAGGGTTCCAAAGCTACA
                                                                                                                                                        1038 AAATATCTCCCTTCACAGGATATTTGTCTCTTATTGAGATCTATCCTTGAATACTGACGC
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/protein id="BAC58011.1"
/db_xref="G1:28804592"
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/db_xref="texaon;46348"
/db_line="Ak-1"
/note="cloning vector: lambda ZapII-cultured
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      CACAGCCATAGCCATGGCCAACCCATTACTTTTCAGAGTTGGTGTCAATTCTACAAGTC
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                                                                                       209 CCACCAACTAAAACTCGTCAGGGCCACACATGCGTTATCTAGCACACAATGGATTC
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INKDSDSLSNFQDAMAADSRLFKLAIQENKHVPEGLESLVDVAGGTGGVAKLHEREFP
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NSKEAISHKGKDGKVIIIDISIDENSDDRGLTELQLEYDVWLTMFLGKERTKKEWEK
LIYDAGFSRYKITPIGGFKSLEVYP
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Vicleae,
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/function="pisatin biosynthesis; catalyzes the
methylation of (+)6a-hydroxymaackiain to (+)pisatin"
/note="methyltransferase"
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Isolation of the cDNAs encoding (+)6a-hydroxymaackiain
3-O-methyltransferase, the terminal step for the synthesis ophytoalexin pisatin in Pisum sativum
Plant Mol. Biol. 35 (5), 551-560 (1997)
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Wu,Q., Preisig,C.L. and VanEtten,H.D.
Direct Submission
Submitted (04-SEP-1996) Plant Pathology, Univ
Forbes Building, Room 204, Tucson, AZ 85721,
Location/Qualifiers
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Pred. No. 1.1e-62;
0; Mismatches 424;
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207 ICCCACCAACTAAAACTCGTCAGGTGCAGAGCCTCATGCGTTATCTAGCACACAATGGAT 26	Oy 267 TCTTTGAGATAGTAAGAATCCATGAGAAGAATAGAAGCATAIGCTCTCACTGCTTCAG 326 104372 TCTTCGCAATTGTGAAGATAGACGACAAGAAGCATAIGCTCTTTCTCCAACTCAA 104313 Qy 327 AGTTACTTGTCAAAGCAGTGAGCTTAGTTTAGTTGAGTGAG	387 CAAATTGTCAAGGTGCATGGAACCAGTTGAAGAGGTGGGTTCATGAGGAAGATCTCACAG 446 	CY 447 TAITIGAGGTCTCCTTAGGAACACCTTTTGGGACTTTATCAATAAAGACCCTGCATATA 506 DD 104192 TCTTGAGACTCCATTATGGGATTAATTTTACAAAATCGACTCATT 104145 CY 5.07 ACAAGTCATTCAATGAGGCAATGGCTTGTGATTCTCAGATCTTGAACTTTAGAG 566 HIND 104144 CAAAGTCATTCAATGAGGCAATGGCTTGTGATTCTCAGATCTTGAACTTTGAACGTTTAGAG 566	104084 627	104024 ACACTGITAAAATIATIGIGAGGGGTTTCCTACGTTAAATGTATAGGTGTCGACCTTC 687 CAAATGTTGGGAAAATTGTCAGGAACAACAAATTGACATTTGTTGGTGGGGACATGT 687 CAAATGTTGTGAAAATTGTCAGGAACAACAATTTGACATTTGTTGTTGGTGGGGACATGT 103964 CAAACGTGGTAAAGGATTAACGGGAAATAACTATCTGATTTTGTAGGCGGAAAAGGT 747 TTAAATGCATCCCAAGGCTGATGCAGGTTCTGCTTA	103844 CAIGCAITAITAAATAGCITAGITICCIGAITCITGAIACAITGAATCCIAAAAATACCA 783	OSS ANABOGGARAGISTICITATION AND CONTRACTOR AND CONTRACTOR SZZ 103664 AAAGAAGGAATCTATAATAGATTTTGTGATAATGAGAGGAGGAGGAGGAGGA	983 AGAAAAGAAGATTGGAAGAAACTCTTCATGGAAGCAGGGTTCCAAAGCTACAAAATA 1042 103544 AGAGATGAAAAAGCATGGAAGAAAATCATCACTGAAGCATTCCAAGCTTACAAAATA 103488 1043 TCTCCCTTCACAGGATATTTGTCTCTTATTGAGATCTTACTAATA 1090 103484 TTTCATATTGGTTTCAAATCACTTATTGAACTTTGTTTTAATTA 103437	RESULT 10 AB091686 LOCUS AB091686 DEFINITION Lotus japonicus H14'OMT mRNA for S-adenosyl-L-methionine:
SOURCE Medicago truncatula (barrel medic) ORGANISM Medicago truncatula Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,	Medicago. 1 (bases 1 to 111587) Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,Eock,D., Kim,D. and Roe,B.A. Medicago truncatula BAC Clone mth2-11a20	KEFERENCE 2 (bases 1 to 11587) AUTHORS Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B., COOK,D., Kim,D. and Roe,B.A. TITLE Direct Submission JOURNAL Submission TORNAL Submitter (129-COT-2002) Department Of Chemistry And Biochemistry, The Intersective of Objective Configuration and State of State	3019, USA bases 1 to 111587) 11,S., Lin,S., Dixon,R., May,G., Sumner,L., ,D., Kim,D. and Roe,B.A. ct Submission Department of Chemistry	The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, COMMENT OK 73019, USA COMMENT ON Jun 7, 2003 this sequence version replaced gi:30061413.	* NOTE: This is a "working draft, sequence. It currently * consists of 3 contigs. Gaps between the contigs * are represented as runs of N. The order of the pieces * is believed to be correct as given, however the sizes * of the gaps between them are based on estimates that have * provided by the submittor. * This sequence will be replaced * by the finished sequence as soon as it is available and * the accession number will be preserved. * the accession number will be preserved.	* 9682	mth2-11a20" T 37516 a 18138 c 18553 g 37160 t 220 others atch atch cal Similarity 58.8%; Pred. No. 2.7e-62;	Matches 699; Conservative 0; Mismatches 347; Indels 142; Gaps 3; QY	Qy 147 TCCACAGCCATGCCATGCCATGCCATACTTTTCAGAGTTGGTGTCAATTCTACAGA 206

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KEWEKLIYDAGFSCYFFSLIEVFP"
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Masshir. Aoki.T. and Ayabe,S.
Direct Submission
Submitted (14-SEP-2002) Shin-ichi Ayabe, Nihon University,
Department of Applied Biological Sciences; Kameino 1866, Fujisawa,
Kanagawa 252-8510, Japan (E-mail:ayabe@brs.nihon-u.ac.jp,
Tel:81-466-84-3703, Fax:81-466-80-1141)
Location/Qualifiers
                                                                                                                 Lotus japonicus
Lotus japonicus
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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7,4'-trihydroxyisoflavanone 4'-0-methyltransferase, complete
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protein id="BAC58013.1"
db_xref="GI:28804596"
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Plant Cell Physiol. 44 (2), 103-112 (2003)
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/strain="MG-20 Miyakojima"
/db_xref="taxon:34305"
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AV407445."
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DNA Res. 7 (2), 127-130 (2000)
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A., Weiss, D.,
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Lavid, N., Wang, J., Shalit, M., Guterman, I., Bar, E., Beuerle, T.,
Menda, N., Shafir, S., Zamir, D., Adam, Z., Vainstein, A., Weiss, D.,
Pichersky, E. and Lewinsohn, E.
                                                 463, AGGAACACCTITCTGGGACTTTATCAATAAAGACCCTGCATATAACAAGTCATTCAATGA
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O-methyltransferases involved in the biosynthesis of volatile phenolic derivatives in rose petals
Plant Physiol. 129 (4), 1899-1907 (2002)
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S Mbeguie-A-Mbeguie,D., Gomez,R.-M. and Fils-Lycaon,B.
Sequence of an O-Methyltransferase from Apricot Fruit (Accession Sequence of East Description of Expression During Fruit Ripening (PGR97-118)
L. Plant Physiol. 114, 1569 (1997)
LE 2 (bases 1 to 1257)
S Mbeguie A Mbeguie,D., Gomez,R.-M. and Fils-Lycaon,B.
Direct Submission
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HGQPWTLSELVSALPISPTKAHFIPRLMRILVHSGFFAKESLSGCGEQGYILTDASAL
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HPFRDAMASDAQLISSLVIDDCKEPGGVDSLVDVGGGTGTVAKSIADAFPHMKCTV
LDLPHVVADLKGSKULSYVAGNPFRAYPADAIFLKWILHDWSDESCVKILERCKAAV
TREGKKGKVIIVEMTVENKYTDKESGETQLFPDHIMWNSTGKERNBKENAKLESDAG
  25-SEP-1997
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                                                                                                                                     Prunus armeniaca
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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/tissue_type="fuit mesocarp and ofdev_stage="ripe"
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ilarity 57.5%; Pred. No. 4.8e-59;
Conservative 0; Mismatches 439;
                       Prunus armeniaca methyltransferase mRNA,
mRNA
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/mol_type="mRNA"
/strain="Bergeron"
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/product="methyltransferase"
/protein_id="AAB71213.1"
/db_xref="GI:2282586"
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Spermatophyta; Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I., Rosales, Rosaceae, Rosoideae, Rosa.
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Characterisation of a novel O-methyltransferase involved in the biosynthesis of 3,5-dimethoxytoluene and 1,3,5-trimethoxybenzene, two major scent components of rose flowers
                                                          GATGATTGCAAAGGAGTGTTTGAGGGATTAGAGGTCATTGGTCGATGTTGGAGGTGGTACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosa chinensis mRNA for orcinol O-methyltransferase A439742. A1:27527923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon start=1
/product="orcinol O-methyltransferase"
/protein_id="CAD29459.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oomt2 gene, orcinol O-methyltransferase.
Rosa chinensis
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/mol_type="mRNA"
/cultivar="01d Blush"
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Cock, J.Mark.
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TFWDYGNHQPSIAHLFNDAMASDARLVTSVIIDDCKGVFEGLESLVDVGGGTGTVAKA
IADAFPHIECTVLDLPHVVADLQGSKNLKYTGGDMFEAVPPADTVLLKWILHDWNDEE
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EKEWAKLFTDAGFSDYKITPILGLRSLIEVYP"
270 c 265 g 329 t
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SAIQLGIPDIINKHGPMTLSELTSALPIHPTKSHSVYRLMRILVHSGFFAKKKLSKTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCAAATTGTCAAGGTGCATGGAACCAGTTGAAGAGGTGGGTTCATGAGGAAGATCTCACA 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88
                             Submitted (15-APR-2002) Vegetables Crops, Newe Ya'ar Research Center, Agricultural Research Organization, P.O. Box 1021, Ramat Yishay 30095, Israel Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function="catalyzes the S-adenosylmethionine-dependent O-methylation of 3-methoxy, 5 hydroxytoluene to form 3,5-dimethoxytoluene (orcinol dimethyl ether)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATGGAGAGCATTCCAACGAGCTACTTCATGCTCAAGCCCACATCTGGAACCACATCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 AGCTTCATAAACTCCATGTCCCTCAATCTGCAATTCAACTAGGTATACCAGATATCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89 GGCTTCATAGATTCTAAGTGTCTAAAATGGATGGTTGAGCTTGACATACCCGACATAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACAGCCATAGCCATGGCCAACCCATTACTTTTCAGAGTTGGTGTCAATTCTACAAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/product="orcinol O-methyltransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 302.8; DB 8;
Pred. No. 2.1e-58;
); Mismatches 442;
                                                                                                                                                                           /organism="Rosa hybrid cultivar"
/mol_type="mRNA"
/culfivar="fragrant Cloud"
/isolate="fc0895"
/db_xref="taxon:128735"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATGGCCGTAAAGCAAGTGAGATTTTTCAAGGTCAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein_id="AAM23005.1"
db_xref="G1:20514369"
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TCAATTGAAACGCAGCTGTTCTTCGACATGCTGATGATGGCCCTCGTCAGAGGACAAGAA 1015
                                                                                                                                                                                               AGGAATGAGAATGAGATTAAGTTTTTCACTGATGCTGGTTTCAGTGATAAGATA 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                  PLN 14-AUG-2002
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AIADAFPHIECTVLDLPHVVADLQGSKNLKYTGGDMFEAVPPADTVLLKWILHDWSDE
ECIKILERSRVAITGKEKKGKVIIIDMMMENQKGDEESIETQLFFDMLMMALVGGKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="orcinol O-methyltransferase"
protein_id="aAM23004.1"
|db_xref="GI:20514367"
|translation="MBRLNSFRHLNOKWSNGEHSNELLHAQAHIWNHIFSFINSMSLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAIQLGI PDI INKHGYPMTLSELTSALPIHPTKSHSVYRLMRILVHSGFFAKKKLSKT
DEEGYTLTDASQLLLKDHPLSLTPYLTAMLDPVLTNPWNYLSTWFQNDDPTPFDTAHG
                                                          GTTACTGAACTAAAGCTCCTTATGGATGTACACATGGCATGTATTAATTGAAAAAGAG 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosa hybrid cultivar
Rosa hybrid cultivar
Rusaryca, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnaliophyta, eudicotyledons, core eudicots,
rosids, eurosids 1, Rosales, Rosaceae, Rosoideae, Rosa.
       896 AAGAAAGGCAAGGTGATTATCATAGATATGATGGAGAACCAGAAGGGGGGATGAGGAA 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (15-APR-2002) Vegetables Crops, Newe Ya'ar Research Center, Agricultural Research Organization, P.O. Box 1021, Ramat Yishay 30095, Israel Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /function="catalyzes the S-adenosylmethionine-dependent O-methylation of orcinol (3,5-dihydroxytoluene) to form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (base 1 to 1252)
Lavid, N., Wang, J., Shalit, M., Guterman, I., Bar, E., Beuerle, T., Menda, N., Shafir, S., Zamir, D., Adam, Z., Vainstein, A., Weiss, D., Pichersky, E. and Lewinsohn, E.
O-methyltransferases involved in the biosynthesis of volatile phenolic derivatives in rose petals
Plant Physiol. 129 (4), 1899-1907 (2002)
                                                                                                                                                           AGAAAAGAAGAAGATTGGAAGAAACTCTTCATGGAAGCAGGGTTCCAAAGCTACAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guterman,I., Bar,E., Beuerle,T.,
, Adam,Z., Vainstein,A., Weiss,D.
                                                                                                                                                                                                                                                                                                                                                                                                                             1252 bp mRNA linear PLN 14-AUG cultivar orcinol O-methyltransferase (OOMI) mRNA,
                                                                                                                                                                                                                                                                                                1076 ACTCCCATTTTGGGTTTAAGGTCTCTTGAGGTTTATCCTTGATAATT 1125
                                                                                                                                                                                                                                                       1043 TCTCCCTTCACAGGATATTTGTCTCTTATTGAGATCTATCCTTGAATACT 1092
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/organism="Rosa hybrid cultivar"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 1252)
Lavid,N., Wang,J., Shalit,M., Guterman,I
Menda,N., Shafir,S., Zamir,D., Adam,Z.,
Pichersky,E. and Lewinsohn,E.
Direct Submission
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/cultivar="Fragrant Cloud"
/isolate="fc0496"
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1. .1252
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                         /translation="MERLINSFKHLNOKWSNGEHSNELLHAQAHIWNHIFSFINSMSLK
SADGATSPININKHGPWILSELTSALPHPTKRASVYRLMRIIJUHSGFFRKKKLSKTD
EEGYTYLTDASQLLLLASLTPFLJAALDPVLTTPWNYLSTWFQNEDPTPFTAHGM
TFWDYGWHQDSIAHLFNDAMASDARLVTSVIIDDCKGVPEGLESLVDVGGGTGTVAKGM
TFWDYGWHQDSIAHLFNDAMASDARLVTSVIIDDCKGVPEGLESLUVGGGTGTVAKGA
IADAPPHIECTVLDLAPHVADLGGSKVIKTGGDMFBAVPPADTVLLKWILHGWNDEE
CKILKKSRYAITSGRKGKVIIIDDWMMENQKGDEESIETQLFFDMLMAALVRGGERN
EKEWAKLFTDAGFSDYKITPILGLRSLIEVYP"
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                                                                                                                                                                                                                                                                           Length 1265;
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/db xref="GI:27527924"
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/gene="comt1"
/gene="comt1"
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/product="cozinol O-methyltransferase"
/protein_id="CaD29459.1"
/brotein_id="CAD29459.1"
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids 1, Rosales, Rosaceae, Rosoideae, Rosa.
1 (bases 1 to 1275)
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Characterisation of a novel O-methyltransferase involved in the biosynthesis of 3,5-dimethoxytoluane and 1,3,5-trimethoxybenzene, two major scent components of rose flowers
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O-methyltransferase
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Cock, J.Mark.
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                         Length 1252,
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                   Score 302.4; DB 8;
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DNA encoding a tob
Maize caffeic O-me
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
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Scybean caffeic ac
DNA encoding a bif
Sweetgum bifunctio
Human GDP-mannose
Human GDP-mannose
Human GDP-mannose
Maize caffeic O-me
Medicago sativa ca
Alfalfa COMT clone
Arabidopsis thalia
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Human GDP-mannose
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CDNA encoding Seque
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                                                                                                                                                                                                                                                                                  L. styraciflua ang
Eucalyptus grandis
cDNA encoding (iso
                                                                                                                                                                                                                                                                                                            Clarkia breweri IE
Eucalyptus grandis
P. sylvestris PMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O-methyltransferase, soybean, degradation, daidzein, flower colour, growth, pollination, irradiation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycine max isoflavone O-methyltransferase clone srl.pk0015.b4.
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/product= lsoflavone_O-methyltransferase
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ABZ14777
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AAA68014
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                                                                                                                                                                                                                                                                                                                                                                                                    AAA29322 standard; cDNA; 1160 BP
 99WO-US30338
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Falco SC;

Fader GM,

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Genetically manipulating biologically active 4'-O-methylated isoflavonoid for producing plants with increased disease resistance, and for accumulation of 4'-O-methylated isoflavonoid nutraceuticals in
                 GCTGAAATGCATGCTTGCAACGTCCAAATGTTGTGGAAAATTTTGTCAGGAAGCAACAA
                                                                                                                                                            TAAGTIGGITTTTACATAATIGGAATGACAACGATTGCATGAAGATATTAGAAATTGTAA
                                                                                                                                                                                                     AGAAGCTATTTCAGGTGAAAGCAAAACAGGAAAAGTAGTTGTCATAGATACTGTGATAAA
                                                                                                                                                                                                                                  AGAAGCTATTTCAGGTGAAAGCAAAACAAGGAAAAGTAGTTGTCATAGATACTGTGATAAA
                                                                                                                                                                                                                                                                                                                                                   TCCTTGAATACTGACGCTGCAATATTCCATTTAGTAGTTAATTTGCATGTTATCAATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alfalfa; isoflavone 4'-0-methyl transferase 8; IOMT; transgenic plant;
                                                                                          TTTGACATTTGTTGGTGGGGACATGTTTAAATGCATCCCCAAGGCTGATGCAGTTCTGCT
                                                                                                                                                                                                                                                                            CGAAAACAAAGATGAGCGCCAAGTTACTGAACTAAAGCTCCTTATGGATGTACACATGGC
                                                                                                                                                                                                                                                                                                               CGAAAACAAAGATGAGCGCCAAGTTACTGAACTAAAGCTCCTTATGGATGTACACATGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCCTTGAATACTGACGCTGCAATATTCCATTTAGTAGTTAATTTTGCATGTTATCAATAAA
The present sequence is isoflavone 4'-0-methyl transferase 8 (IOMT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alfalfa isoflavone 4'-O-methyl transferase 8 coding sequence
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                                                                                                                                                                      were prepared from soybean embryo (19 days after flowering), root, 8-day old root and seed (15 days after flowering).

Soflavon enethyltransferase catalyses the first step in degradation of daidzein. Suppression of this enzyme will yield higher concentrations of this beneficial isoflavone in, e.g. soybean seed. Flavonoids serve as co-pigments in flower colour, stimulate pollen tube growth, attract pollenators, act as feeding deterrents and protect against UV irradiation in fruits and seeds. The cDNA and proteins can be used to isolate homologues, for immunological screening and for positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99
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                                                                 polynucleotide encoding flavonoid biosynthetic enzymes for creating isgenic plants and for immunological screening of cDNA libraries
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                                                                                                                                                          AAA29321-25 encode isoflavone O-methyltransferases isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1160; DB 21; Length 1160;
Pred. No. 3.4e-295;
Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1160 BP; 361 A; 197 C; 254 G; 348 T; 0 other;
                                                                                                                       2; Page 32; 39pp; English
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Matches 1160; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coding sequence from Alfalfa. The present invention relates to a method for genetically manipulating the level of biologically active IOMT. The method involves transforming the target plant with a DNA fragment (the present sequence) to form a transgenic plant. IOMT is useful as foodstuff, nutritional supplement, animal feed supplement, nutraceutical and as a pharmaceutical. Transgenic expression of IOMT in legumes is useful for engineering both phytoalexin levels for improved disease resistance, and health promoting nutraceutical phytochemicals. IOMT is useful for engineering isoflavone 4 "O-methylation, or other organisms, that do not naturally produce isoflavonoids.
                                                                                                                                                                                                                                                                                                                         88
                                                                                                                                                                                                                                                                                                                     cricarcaarraarggccgaaaaccaagrgaaarrrrcaaagcacaagcrrraraaraca
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                                                                                                                                                                                                                      DB 22; Length 1231;
                                                                                                                                                                                                                                                                                        CTICATIAAACAAIGGCCGIAAAGCAAGIGAGAITITICAAGGICAAGC
                                                                                                                                                                                                                   Score 645.4; DB 22; Length
Pred. No. 9.7e-160;
0; Mismatches 251; Indels
                                                                                                                                                                                     Sequence 1231 BP; 402 A; 183 C; 235 G; 411 T; 0 other;
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Isoflavone O-methyltransferase catalyses the first step in degradation of daidzein. Suppression of this enzyme will yield higher concentrations of this beneficial isoflavone in, e.g. soybean seed. Flavonoids serve as co-pigments in flower colour, stimulate pollen tube growth, attract pollenators, act as feeding deterrents and protect against UV irradiation in fruits and seeds. The CDNA and proteins can be used to isolate homologues, for immunological screening and for positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA29321-25 encode isoflavone O-methyltransferases isolated from various soybean (Glycine max) tissues. CDNA libraries se4, sr1, srr1c and ss11c were prepared from soybean embryo (9) days after flowering), root, 8-day old root and seed (25 days after flowering).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide encoding flavonoid biosynthetic enzymes for creating transgenic plants and for immunological screening of cDNA libraries
                                                                                                917 ATCAAGTTACTCAAATTAAGCTCCTTATGGATGTAAAACATGGCTTG---TCTAAATGGAA
858 AAAGCAAAACAGGAAAAGTAGTTGTCATAGATACTGTGATAAACGAAAACAAAGATGAGC
                                   AAGAGAGAAAAAGAAGATTGGAAGAACTCTTCATGGAAGCAGGGTTCCAAAGCTACA
                                                                                                                                                                                    974 AAGAGAAAATGAGGAAGAATGGAAGAAACTCTTCATAGAAGCTGGTTTCCAACACTATA
                                                                                                                                                                                                                                                              1034 AGATATCTCCTTTGACTGGATTTTTGTCTTTATTGAGATCTATCCATAAACACTTTTGC
                                                                          918 GCCAAGTTACTGAACTAAAGCTCCTTATGGATGTACACATGGCATGTATTATTAATGGAA
                                                                                                                                                                                                                           AAATATCTCCCTTCACAGGATATTTGTCTCTTATTGAGATCTATCCTTGAATACTGACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycine max isoflavone O-methyltransferase clone ssllc.pk002.dl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        daidzein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O-methyltransferase; soybean; degradation; daidzein.
flower colour; growth; pollination; irradiation; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2..1048
/ttag= a
/product= Isoflavone_O-Methyltransferase
/partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DUPO ) DU PONT DE NEMOURS & CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; cDNA; 1253
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1051 CACAGGATATTTGTCTCTTATTGAGATCTATCCTTGAATACTGACGCTGCAATATTCCAT 1110
                                                                                    1012 crrrestrircasarcretaatreascretarecriasacarararecrasecristrarse 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA29321-25 encode isoflavone O-methyltransferases isolated from various soybean (Glycine max) tissues. CDNA libraries se4, sr1, srr1c and ss11c were prepared from soybean embryo (19 days after flowering), root, 8-day old root and seed (25 days after flowering).

Isoflavone O-methyltransferase catalyses the first step in degradation of daidzein. Suppression of this enzyme will yield higher concentrations of this beneficial isoflavone in, e.g. soybean seed. Flavonoids serve as co-pigments in flower colour, stimulate pollen tube growth, attract pollenators, act as feeding deterrents and protect against UV irradiation in fruits and seeds. The cDNA and proteins can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotide encoding flavonoid biosynthetic enzymes for creating transgenic plants and for immunological screening of cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 CATTAAACAATGGCCGTAAAGCAAGTGAGATTTTTCAAGGTCAAGCTCTCTTGTACAAAC
                                                                                                                                                                                                                                                                                                                                             Glycine max isoflavone O-methyltransferase clone srr1c.pk001.b16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isolate homologues, for immunological screening and for positive selection methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 507.2; DB 21; Length 1065;
Pred. No. 2.2e-123;
0; Mismatches 318; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                           O-methyltransferase, soybean, degradation, daidzein flower colour, growth, pollination, irradiation, ss
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/transl except= (pos:268..279, aa:Glu)
/note= "A 9 bp insertion is present"
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                                                                                                                         1111 TTAGTAGTTAATTTGCATGTTATCA 1135
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Best Local Similarity
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Flavonoid;
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                                     Sequence 1253 BP; 374 A; 232 C; 267 G; 380 T; 0 other;
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Isoflavone O-methyltransferase catalyses the first step in degradation of daidzein. Suppression of this enzyme will yield higher concentrations of this beneficial isoflavone in, e.g. soybean seed. Plavonoids serve as coligments in flower colour, stimulate pollen tube growth, attract pollenators, act as feeding deterrents and protect against UV irradiation in fruits and seeds. The CDNA and proteins can be used to isolate homologies, for immunological screening and for positive
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Glycine max isoflavone O-methyltransferase clone srr1c.pk001.b16.
                                                                     Isoflavone O-methyltransferase; soybean; degradation; daidzein; Flavonoid; flower colour; growth; pollination; irradiation; ss.
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Pred. No. 2.2e-123;
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/note= "A 9 bp insertion is present"
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/*tag= a /product= Isoflavone_O-Methyltransferase /partial

Location/Qualifiers

Falco

GM, Fader

odell JT,

98US-0113190. 99WO-US30338

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old Yook and seed (25 days arter 110002110g).
Isoflavone O-methyltransferase catalyses the first step in degradation of daidzein. Suppression of this enzyme will yield higher concentrations of this beneficial isoflavone in, e.g. soybean seed. Flavonoids serve as co-pigments in flower colour, stimulate pollen tube growth, attract pollenators, act as feeding deterrents and protect against UV irradiation in fruits and seeds. The CDNA and proteins can be used to isolate homologues, for immunological screening and for positive
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                                                                    ATGGAATCTTTGAGATCCATGAGAGCCAAGAAGATCATGAACTAACATATGCTCTAACCC 298
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     21; Length 1053;
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Score 497.8; DB 21; Length
Pred. No. 6.5e-121;
0; Mismatches 317; Indels
  Query Match
Best Local Similarity 68.9%;
Matches 730; Conservative
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Glycine max isoflavone O-methyltransferase clone se4.pk0007.a11

(first entry)

26-SEP-2000

AAA29321

BP.

AAA29321 standard; cDNA; 1053

O-methyltransferase; soybean; degradation; daidzein; flower colour; growth; pollination; irradiation; ss.

Isoflavone (Flavonoid; 1 Glycine max 1

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Gaps

21;

(E-OMT)

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GAGATTTTTCAAGGTCAAGCTCTCTTGTACAACA1TTGCTTGGCTTCATAGATTCTAAG 106
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               preparation
                                                                                          The present sequence encodes norcoclaurine 6-0-methyltransferase Also described is a method for the preparation of the secondary metabolite of a plant derived from coclaurine or reticuline.
                                                                                                                                                                                       Score 209.2; DB 20; Length Pred. No. 6e-45; 0; Mismatches 463; Indels
                useful for
                                                                                                                                                         Sequence 1041 BP; 320 A; 186 C; 245 G; 290 T; 0 other
                norcoclaurine 6-0-methyl-transferase
                                                             Claim 5; Page 12; 27pp; Japanese
                                                                                                                                                                                       Query Match
Best Local Similarity 53.6%;
Matches 558; Conservative
                               secondary plant metabolite
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                                                                                      944 ATGGATGTACACATGGCATGTATTATTAATGGAAAAGAGAAAAAAGAAGAAGATTGGAAG 1003
                                                                                                                                                                                                                                               AAGCTCATCCATGCAGGGTACAAAGGGCATAAGATAACACAAAATTACTGCTGTACAA 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This cDNA encodes a polypeptide having the enzymatic activity of (S)-3, -hydroxy-N-methylcoclaurine 4'-0-methyltransferase (4'-OMT). A vector containing the DNA can be used to transform a microbe for the recombinant preparation of the enzyme. The enzyme can be used to prepare a secondary metabolite of a plant derived from reticuline which is useful as a raw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116
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GTCGACATTGTCTTAAATGTGCAATCAGAACATCCTTA---TACCAAGATGAGACTGACT 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA.
                                                                                                                                     898 TIGGATTIGGACATGATGCTCAACACIGGAGGAAAAGAGAGAGCACTGAAGAGGAATGGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (S)-3'-hydroxy-N-methylcoclaurine 4'-0-methyltransferase; 4'-OMT; enzyme; secondary metabolite; reticuline; drug; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 178.4; DB 20; Length 1050;
Pred. No. 7.7e-37;
0; Mismatches 481; Indels 21;
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                                                                                                                                                                                                                                                                                                    TCTCTTATTGAGATCTATCCTT 1085
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ilarity 51.3%;
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P-PSDB; AAY27183.
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The invention relates to a composition comprising a human GDP-mannose 4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying GM4,6D inhibitors. GM4,6D inhibitors are useful for reducing inflammation in a mammalian subject and for treating or ameliorating diseases affected by the level of cellular fucosylation or diseases affected by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAGTTTTGAGGGGCTAGATTCCATGGTGGATGTTGGTGGTGGAACTGGAACCACGGCC 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 AGAATTATCTGTGACGCATTTCCTAAGTTGAATGTGTTGTGCTTGACCTTCCTCTGTT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTAGAGAACTTGACAGGGACCAATAATTTGAGTTTTGTTGGTGGTGACATGTTCAACTCT 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fucosylation of glycoconjugates. These diseases include arthritis, transplant rejection, asthma, sepsis, reperfusion injury, stroke or infection. The GW4,6D peptide or a polynucleotide encoding it is also useful for manufacturing complex carbohydrates and as targets for screening small molecule antagonists of the activity of the enzyme. The polynucleotide is useful in developing an assay for defects in the enzyme, as well as in gene replacement therapy. Sequences ABX17944 and ABX17747-ABX33716 represent DNA molecules encoding human GM4,6D peptides of the invention.
  cellular fucosylation; glycoconjugate fucosylation; transplant rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide, for manufacturing complex carbohydrates, or as targets for screening GM4,6D antagonists for treating e.g. arthritis, or transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               515 TTCAATGAGGCAATGGCTTGTGATTCTCAGATGTTGAACTTGGCGTTTAGAGATTGCAAT
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                   arthritis; asthma; sepsis; reperfusion injury; stroke; infection; complex carbohydrate; gene replacement therapy; immunosuppressive; antiinflammatory; antiarthritic; antibacterial; cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D)
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76.9%; Pred. No. 9.5e-32;
Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 256 BP; 61 A; 49 C; 65 G; 81 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 13958; 6pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                    97US-0984246.
98US-0149674.
99US-0333177.
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                                                                                        antiasthmatic, vasotropic
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                                                                                                                                 Homo sapiens
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09-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sullivan F,
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                                                                                                                                                                                  Human, GDP-mannose 4,6-dehydratase, GM4,6D; gene; ss; inflammation; cellular fucosylation; glycoconjugate fucosylation; transplant rejection; arthritis; asthma; sepsils; reperfusion injury; stroke; infection; complex carbohydrate; gene replacement therapy; immunosuppressive; antiinflammatory; antiarthritic; antibacterial; cerebroprotective;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enzyme, as well as in gene replacement therapy. Sequences ABX17942-ABX17944 and ABX17947-ABX33716 represent DNA molecules encoding human GM4,6D peptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D) peptide, for manufacturing complex carbohydrates, or as targets for screening GM4,6D antagonists for treating e.g. arthritis, or transplant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72; Indels
                                                                                                                                                  Human GDP-mannose 4,6-dehydratase (GM4,6D) DNA #5575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 266 BP; 91 A; 42 C; 60 G; 73 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 5577; 6pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at segdata.uspto.gov/sequence.html
                                   ВР
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                                   ABX23518 standard; cDNA; 266
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98US-0149674.
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                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                     antiasthmatic; vasotropic.
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                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                   15-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rejection
                                                                           ABX23518;
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RESULT 10
                   ABX23518
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Gaps

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RESULT 11 ABX19667 260

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198

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259 ATGGAATCTTTGAGATCCATGAGAGCCAAGAACATGAACTAACATATGGTCTAACCC 318
enzyme, as well as in gene replacement therapy. Sequences ABX17942-ABX17944 and ABX17947-ABX33716 represent DNA molecules encoding Muman GM4.6D peptides of the invention.

Note: The sequence data for this of the printed specification but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 ACATAAT----ACAGAACCATGCCAAACCCATTTCTCTTTCTGACTTGGTCTCTACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 rrcaaarrccaccagcraacccrerrrcrecaccacricarecerrerrescacaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 ATGGATTCTTTGAGATAGTAAGAATCCATGACAAAAAA---AGCATATGCTCTCACTG
                                                                                                                                                                                                                                                                                           21 CATTAAACAATGGCCGTAAAGCAAGTGAGATTTTTCAAGGTCAAGCTCTCTTGTACAAAC
                                                                                                                                                                                                                                                                                                                                                                                 81 ATTIGCTIGGCTICATAGATICTAAGIGICTAAAAIGGAIGGIIGAGCIIGACAIACCCG
                                                                                                                                                                                                                                                                                                                                                                                                                           85 AGCTATATGGGCACCTAAGACCTATGTGTCTTAAGTGGGCTGTTCAACTAGGTATTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 ACATAATCCACAGCCATAGCCATGGCCAACCCATTACTTTTCAGAGTTGGTGTCAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TACAAGTCCCACCAACTAAAACTCGTCAGGTGCAGAGCCTCATGCGTTATCTAGCACACA
                                                                                                                                                                                                                                                                                                                                     25 cricaargaaraaccaaaaagaaarrgagcrerrrgaggggggaarcrergracarg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maize; corn; caffeic O-methyltransferase; lignin; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGCTTCAGAGTTACTTGTCAAAAGCAGTGAGCTTAGTTTAGCTCCAATGGTT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    crecarcaaserrerrercaarasrasrasrcarrerererereresaresrr
                                                                                                                                                                                                   Score 142.2; DB 25; Length 381; Pred. No. 1.8e-27;
                                                                                                                                                                                                                                             0; Mismatches 108; Indels
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                                                                                                                                                         Sequence 381 BP; 109 A; 88 C; 69 G; 115 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      caffeic O-methyltransferase cDNA.
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139..1266
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                                                                                                               at seqdata.uspto.gov/sequence.html.
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97US-0057082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                               236; Conservative
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                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          318
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                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                          940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; GDP-mannose 4,6-dehydratase; GM4,6D; gene; ss; inflammation; cellular fucosylation; glycoconjugate fucosylation; transplant rejection; arthritis; asthma; sepsils; reperfusion injury; stroke; infection; complex carbohydrate; gene replacement therapy; immunosuppressive; antlinflammatory; antiarthritic; antibacterial; cerebroprotective;
                                                820
                                                                                                                                  880
                                                                                                                                                                              181
                                                                                                                                                                                                                                                                    241
                                                                                   CAAGCIGAIGCAGIGCIACIAAAGIGGGIITITACAIAATIGGACCGACGAAAAIIGCAIA 121
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AACTIGACAGGGACCAATAATITGAGTITTTGTTGGTGGTGACATGTTCAACTCTATCCCT
                                              761 AAGGCIGATGCAGTICTGCTTAAGTTGGTTTTACATAATTGGAATGACAACGATTGCATG
                                                                                                                                    AAGATATTAGAAAATTGTAAAGAAGCTATTTCAGGTGAAAGCAAAACAGGAAAAGTAGTT
                                                                                                                                                              GTCATAGATACTGTGATAAACGAAAACAAAGATGAGCGCCCAAGTTACTGAACTAAAGCTC
                                                                                                                                                                                                                                                                  <u> arcaragarecceraaraaareaaeeragareacceegarareacaaacaaaeerr</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human GDP-mannose 4,6-dehydratase (GM4,6D) DNA #1724.
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                                                                                                                                                                                                                                                                                                              CTTATGGATGTACACATG 958
                                                                                                                                                                                                                                                                                                                                                        242 AGTITGGACATTATTATG 259
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97US-0984246.
98US-0149674.
99US-0333177.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-066673/06.
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09-SEP-1998;
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                                                                                                                                  821
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                                                                                                                                                                                                                        881
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WPI; 1999-204667/17. P-PSDB; AAY05661.

RESULT 13

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This DNA sequence encodes a caffeic O-methyltransferase (see AAY05661)

of maize. A polynucleotide having this sequence can be amplified from a cDNA library prepared from premeiotic to uninucleate tassel from a cDNA library prepared from premeiotic to uninucleate tassel AAX25226. The invention provides methods and compositions relating to altering light biosynthesis and/or the light composition of plants. Isolated nucleic acids (see AAX25196-16) that code for proteins (see AAY05657-77) involved in lighth biosynthesis are claimed. Also claimed are recombinant expression cassettes, host cells (especially maize or sorghum), and transgenic plants and cells (especially maize or sorghum), and transgenic plants and cells (especially maize or sorghum), and transgenic plants and transforming a plant cell with a recombinant expression cassette comprising a lighth biosynthesis A claimed method involves transforming a plant cell with a recombinant expression cassette comprising a lighth biosynthesis polynucleotide operably linked to a promoter, growing the plant cell under plant growing conditions, and inducing expression of the polynucleotide for a time sufficient to modulate (preferably increase) lighth biosynthesis in the plant. The plant lighths can be used as chemical feedstock. Plant material of increased lighth content can be used as a fuel source, and in the pulp and paper industry. Decreased lightin content and in the pulp and paper industry.
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                             Nucleic acids encoding plant lignin biosynthesis enzymes - used to
transform plants to modulate lignin biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 10.4%; Score 120.2; DB 20; Length 1412; Best Local Similarity 54.0%; Pred. No. 1.8e-21; Matches 292; Conservative 0; Mismatches 243; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1412 BP; 324 A; 400 C; 375 G; 313 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and in the pulp and paper industry. Decrea improves the digestibility of fodder crops.
                                                                                                                  Claim 2; Page 119-121; 166pp; English.
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The invention relates to methods for producing forage legumes or woody plants having altered lignin composition. Methods for transforming forage legumes with a DNA construct comprises alfalfa caffein acid 3-0. methyltransferase (CCOMT) enzyme or its fragment under a lignification-associated tissue specific promoter, resulting in the down regulation of the corresponding proposesion. The methods are useful for down-regulation of the suppression. The methods are useful for down-regulation of the corresponding homologous OMT genes, gene silencing, reduced OWT activity levels, reduced lignin content, and modified lignin composition in transgenic plants, and increased digestibility of transgenic plant materials in ruminant animals. The expression of CCOMT transgene produces the transformed plant and greatly improved forage in vivo digestibility, and for making lignins with altered dimer bonding patterns. Transforming forage legumes with all all the produce plants having modified lignin content and account of the content of the content plants having modified lignin and content in the produce plants having modified lignin and content and account of the content plants having modified lignin and content and account of the content plants having modified lignin and content and content and account of the content plants and plants and plants and plants and account of the content plants and plants and account of the content plants and account of the content plants and plants and account of the content plants and account of the content plants and account of the content plants and account of the content plants and account of the content plants and account of the content plants and account of the content plants and account of the content plants and account of the content plants and account of the content plants and account of the content plants and account of the content plants and account of the content plants and account of the content plants and account of the content plants and account of the content plants and account of th
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                                                                                                                                                                                                                                                Alfalfa, caffeoyl CoA 3-O-methyltransferase, CCOMT; lignin, woody plant, forage legume, transgenic plant, paper industry, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              improve pulping characteristics for the paper industry. The present cDNA sequence encodes alfalfa caffeoyl CoA 3-0-methyltransferase (CCOMT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transforming forage legumes for modifying lignin composition and increasing in vivo digestibility comprises transforming plants with lignin biosynthetic enzyme genes under lignification-associated tissue specific promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Alfalfa caffeoyl CoA 3-O-methyltransferase
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                                                                                                                                                                                         Medicago sativa caffeoyl CoA 3-0-methyltransferase (CCOMT) cDNA.
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                            AAD19546 standard; cDNA; 1098 BP.
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Best Local Similarity 52.7%;
Matches 309; Conservative
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        CCTTAGGAACACCTTTCTGGGACTTTATCAATAAAGACCCTGCATATAACAAGTCATTCA
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                                                                 TCTTTGAGGGACTGGAATCCATTGTGGATGTTGGTGGTGGAACTGGAATCACAGGAAGA
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                                                                                                                                                                                                                                                                                                         TIGIGGCAGAATGCATACTTCCAGTGGCTCCAGATTCAAGCCTGGCCACAAAAGGTGTGG
                                                                                                                                                                                                                                                                                                                              "the inverted complement of this portion
of the COMT gene was the antisense fragment
used to reduce alfalfa lignin content"
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/note= "the inverted complement of this portion
of the COMT gene was the antisense fragment
used to reduce tobacco lignin content"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u> AAAATTTGTCAGGAAGCAACAATTTGACATTTGTTGGTGGGGACATGTTTAAATGCATCC</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                764 AAGAIGCTCCATCTIAICCAGGAGTTGAGCATGTTGGTGGAGACATGTTTGTCAGTATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAAGGCTGATGCAGTTCTGCTTAAGTTGGTTTTACATAATTGGAATGACAATGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 519 ATGAGGCAATGGCTTGTGATTCTCAGATGTTGAACTTGGCGTTTAGAGATTGCAATTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     584 ACAAGGGGAIGTCTGATCACTCTACCATCAAAGAAAATTCTTGAGACCTACACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             644 GTTTTGAAGGCCTTAAATCTCTTGTTGATGTAGGTGGTGGTACTGGAGCTGTAATTAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           639 TIAICIGIGAGGCITITCCTAAGCIGAAATGCATGGTGTTGGAACGICCAAATGTTGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAAAGGCTGATGCTGTTTTTATGAAGTGGATTTGTCATGACTGGAGTGATGAGGCACTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         579 TCTTTGAGGGACTGGAATCCATTGTGGATGTTGGTGGTGGAACTGGAATCACAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alfalfa COMT clone pCOMT1, obtained from a cDNA library in lambda ZAP II, was the basis of antisense genes used to reduce the lignin content of E.g. tobacco and alfalfa.

(Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reducing lignin content in plants - by transfection with an anti-sense gene for caffeic acid 3-0-methyl-transferase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      996 ATTGGAAGAAACTCTTCATGGAAGCAGGGTTCCAAAAGCTACAAAAT 1041
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                                                                                                                                                                                                                                                                 (ROBE-) ROBERTS NOBLE FOUND INC SAMMUEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Page 21-23; 39pp; English
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Local Similarity 52.7%;
es 309; Conservative
94WO-US03356
                                                                                                                                    93US-0045263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1994-333204/41.
P-PSDB; AAR63203.
                                                                                                                                                                                                                                                                                                                                                                                              Dixon RA, Ni W;
      31-MAR-1994;
                                                                                                                                    02-APR-1993;
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990S-0139461

990S-0139462

990S-0139462

990S-0139462

990S-0139763

990S-0139763

990S-0139763

990S-0140835

990S-0140823

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990S-0142980

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990S-0145389

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990S-0147303
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99US-0148171.
99US-0148319.
99US-0148341.
99US-0148685.
99US-0149368.
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99US-0149723.
99US-0149929.
  99US-0139460
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02-AUG-1999;
02-AUG-1999;
02-AUG-1999;
03-AUG-1999;
04-AUG-1999;
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10-AUG-1999;
11-AUG-1999;
12-AUG-1999;
13-AUG-1999;
13-AUG-1999;
16-AUG-1999;
18 - 70x - 1999;

18 - 74x - 1999;

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21 - 74x - 1999;

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23-JUL-1999;
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23-JUL-1999;
26-JUL-1999;
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14-JUL-1999;
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16-JUL-1999;
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19-JUL-1999;
19-JUL-1999;
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20-JUL-1999;
20-JUL-1999;
21-JUL-1999;
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20-AUG-1999;
20-AUG-1999;
                                                                                                                                                                                                                           19-JUL-1999;
  Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                        Arabidopsis thaliana DNA fragment SEQ ID NO: 29270.
         AAC40707 standard; DNA; 1267 BP
                                                                                                                                                                   990S-0121825.
990S-0123180.
990S-0125788.
990S-0125788.
990S-0126785.
990S-0126785.
990S-012824.
990S-0130077.
990S-0130801.
990S-0130821.
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                                        17-OCT-2000 (first entry)
                                                                                                       Arabidopsis thaliana
                                                                                                                       EP1033405-A2
                                                                                                                                                                                                                          06-APR-1999,
16-APR-1999,
19-APR-1999,
19-APR-1999,
23-APR-1999,
23-APR-1999,
28-APR-1999,
30-APR-1999,
30-APR-1999,
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05-MAY-1999;
06-MAY-1999;
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07-MAY-1999;
11-MAY-1999;
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25-MAY-1999;
27-MAY-1999;
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                                                                                                                                      06-SEP-2000,
                        AAC40707;
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734 GGTGGGGACATGTTTAAATGCATCCCCAAGGCTGATGCAGTTCTGCTTAAGTTTGGTTTTA 793 818 GGAGGAGATATGTTTGTAAGTGTCCCTAAAGGTGATGCCATATTCATGAAGTGGATATGT 794 CATAATTGGAATGAACAATGCATGAAGATATTAGAAAATTGTAAAGAAGCTATTTCA 878 CATGACTGGAGTGGACATTGCGTGAAATTCTTGAAAACTGCTACGAGTCACTTCCA

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Gaps
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99US - 0149930,
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Best Local Similarity
Matches 225; Conserv
                                                             26-AUG-1999;
27-AUG-1999;
27-AUG-1999;
27-AUG-1999;
30-AUG-1999;
31-AUG-1999;
07-SEP-1999;
10-SEP-1999;
13-SEP-1999;
13-SEP-1999;
13-SEP-1999;
16-SEP-1999;
                                                                                                                                                                                                                                                                                                                                       23.58F - 1999

28.58F - 1999

29.58F - 1999

06.0CT - 1999

08.0CT - 1999

13.0CT - 1999

13.0CT - 1999

14.0CT - 1999

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16.0CT - 1999

17.0CT - 1999

18.0CT - 1999

19.0CT - 1999

20.0CT - 1999

21.0CT - 1999

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20.0CT                                                                                                                                                                                                                                                                                                   20-SEP-1999;
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Search completed: November 9, 2003, 23:45:31
Job time : 432 secs
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us-09-868-547-3.rni

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NAME/KEY: unsure
LOCATION: (472)
FEATURE:
NAME/KEY: unsure
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ORGANISM: Glycine
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5019.651 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/eDCOMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-08-200-569-3
US-08-288-4
US-09-500-569-11
US-08-91-677-5
US-09-615-192A-174
US-09-615-192A-174
US-09-615-192A-177
US-08-975-316-51
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US-09-615-192A-187
US-09-615-192A-191
US-08-232-463-14
US-09-615-192A-192
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US-09-500-569-13
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Maximum Match 100%
Listing first 45 summaries
                                         OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Sequence 14, Appl
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US-09-500-569-17
US-09-500-569-17
Sequence 17, Application US/09500569
Patent No. 6329204
GENERAL INPERMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
PILE REFERENCE: BB1327 US NA
CURRENT PPLICATION: Plant Caffeic acid 3-O-Methyltransferase Homologs
CURRENT FILING DATE: 2000-02-09
EARLIER FILING DATE: 2000-02-09
MWHER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NOS: 28
SET IND NO 17
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           9.8%;
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Matches 228; Conservative
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US-08-715-325-1
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Matches 313
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                                                                                                                                                                                                                                                             308 CAACGATTGCATGAAGATATTAGAAAATTGTAAAGAAGCTATTTCAGGTGAAAGCAAA 865
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                                                       CACAGCAAAGATTATCTGTGAGGCTTTTTCCTAAGCTGAAATGCATGGTGGTTGGAACGTCC
                                                                                         710 TGTAGTCAACATGATTGTCTCAAAGTATCCCACTATTAAGGGCATTAATTTTGATTTGCC
                                                                                                                         688 AAATGTTGTGGAAAATTTGTCAGGAAGCAACAATTTGACATTTGTTGGTGGGGACATGTT
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LEGRAND, Michel
VENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,288
FILING DATE: 10-MAR.1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EB 9119279.9
FILING DATE: 10-SEP-1991
PRIOR APPLICATION NUMBER: PCT/GB92/01460
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: KOKULIS, Paul N. REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 206860/SEE36543/UST TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CUSHMAN DARBY & CUSHMAN, L.L.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1100 New York Avenue, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5: Floppy disk
IBM PC compatible
3YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08204288
Patent No. 5959178
                                                                                                                                                                                                                                                                                                                                                                                                                                 VAN DOORSSELAERE, Ja
FRITIG, Bernard J.M.
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VAN MONTAGU, Marc
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MOLECULE TYPE: DNA (genomic)
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TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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JOUANIN, Lise
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TITLE OF INVENTION: PL
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
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RY: U.S.A.
20005-3518
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US-08-204-288-1
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                                                                                                                                                                                                                                                                                                                                 567 CAAGGTCTTCAATAAGGGAATGTCTGACCACTCTACCATTACCATGAAGAAGATTCTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 808 CAACGATTGCATGAAGATATTAGAAAATTGTAAAGAAGCTATTTCAGGTGAAAGCAAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  507 ATTINACAAGGCCIATGGGATGACTGCATTTGAATATCATGGCACGGATCCAAGATTCAA
                                                                                                                                                                                                                                                               508 CAAGICATICAAIGAGGCAAIGGCTIGIGAITCICAGAIGIIGAACTIGGCGITITAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                687 IGTCGTTAACACCATCGTCTCTAAATACCCTTCAATTAAGGGCATTAACTTTGATTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                747 ccaccicarreaggargccccarcrrarcccggrgrggaggargrrggrggrgrrgrr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                807 IGTTAGTGCCCAAAGCAGATGCCGTTTTCATGAAGTGGATATGCCATGATTGGAGCGA
                                                                                                                                   448 ATTTGAGGICTCCTTAGGAACACCTTTCTGGGACTTTATCAATAAAGACCCTGCATATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  628 CACAGCAAAGATTATCTGTGAGGCTTTTCCTAAGCTGAAATGCATGGTGTGGAACGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  688 AAATGTTGTGGAAAATTTGTCAGGAAGCAACAATTTGACATTTGTTGGTGGGGACATGTT
                                                                     Gaps
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0
      Length 1368;
                                                                     Indels
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APPLICANT: Tsai, Chung-Jui
APPLICANT: Tsai, Chung-Jui
APPLICANT: Podila, Gopi
TITLE OF INVENTION: Genetic Engineering of Wood Color
TITLE OF INVENTION: in Plants
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COPERATING SYSTEM: MS DOS 6.22 SOFTWARE: WordPerfect for Windows 5.2
Score 109.8; DB 2;
Pred. No. 1.1e-20;
0; Mismatches 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1048 CITCACAGGATATTTGTCTTTTTTGAGATC 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1101 CTGTGCATTCAACACACATGTCATTGAACTC 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Michael, Best & Friedrich
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Patent No. 5886243
9.5%;
                                                              313; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Wisconsin COUNTRY: United
                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Milwaukee
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988 AGAAGAAGATTGGAAGAAACTCTTCATGGAAGCAGGGTTCCAAAAGGTACAAAATATCTCC 1047
                                                                                1057 CGAGAAGAATTTGAGGGCTTAGCTAAGGGAGCTGGCTTCCAAGGTTTTGAAGTAATGTG 1116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTATCTGTGAGGCTTTTCCTAAGCTGAAATGCATGGTGTGGAACGTCCAAATGTTGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                475 ccrargdalargacaccarradaraccarggcacagarccaagarrcaacaagargrica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    535 ACCGTGGAATGTCTGATCACTCCACTATGTCAATGAAGAAGATTCTTGAGGACTACAAAG
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                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09453323
Patent No. 6441272
GENERAL INFORMATION:
APPLICANT: Ve. Zheng-Hua
TITLE OF INVENTION: PLANTS
TITLE OF INVENTION: PLANTS
TITLE OF INVENTION: PLANTS
TITLE REPERENCE: 235.00090101
CURRENT APPLICATION NUMBER: US/09/453,323
CURRENT PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
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53.1%; Pred. No. 2e-20;
ative 0; Mismatches 205;
                                                                                                                                1048 CTTCACAGGATATTTGTCTCTTATTGAGATC 1078
                                                                                                                                                                                 1117 crgrgcarrcaacacargrcarrcaarrc 1147
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US-08-204-288-3
; Sequence 3, Application US/08204288
; Patent No. 5959178
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          879 TTGTCATAGATACTGTG 895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 53.15
Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1507
                                                                                                                                                                                                                                                            RESULT 4
US-09-453-323-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-453-323-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  568 ITGCAATTGGGTCTTTGAGGACTGGAATCCATTGTGGATGTTGGTGGTGGTGGAACTGGAAT 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               643 GACCTACAAAAGGCTTTGAAGGCCTCACGTCCTTGGTGGATGTTGGTGGTGGACTGGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        688 AAATGTTGTGGAAAATTTGTCAGGAAGCAACAATTTGACATTTGTTGGTGGGGACATGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               823 TGTTAGTGTGCCCAAAGCAGATGCCGTTTTCATGAAGTGGATATGCCATGATTGGAGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        448 ATTTGAGGTCTCCTTAGGAACACCTTTCTGGGACTTTATCAATAAAGACCCTGCATATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Populus Tremuloides
DEVELDOPRENTAL STAGE: Gour year old sapling
DEVELOPMENTAL STAGE: undergoing lignification in summer
TISSUE TYPE: secondary xylem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 109.8; DB 2;
Pred. No. 1.2e-20;
0; Mismatches 312;
                                                                                                                                                                                                      NAME: Gemignani, Joseph A
REGISTRATION NUMBER: 19,482
REPERENCE/DOCKET NUMBER: 66040/9627
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 271-6560
TELEPAX: (414) 277-0656
                     APPLICATION NUMBER: US/08/715,325
                                             FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US60/007727
FILING DATE: 30 NOV 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                            TELEFAX: (414) 277-0656
TELEX: 262057
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 1503 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA to total mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 49.6%;
Matches 313; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: cDNA to mRNA HYPOTHETICAL: no
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: no
ORIGINAL SOURCE:
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583 GATCCAAGGTTTAACAAGGTTTTCAACAAGGGAATGGCTGATCACTCTACCATCACAATG 642
704 TIGICAGGAAGCAACTITGACATTTGTTGGTGGGGACATGTTTAAATGCATCCCCAAG 763
                                                                                                                                               764 GCTGATGCAGTTCTGCTTAAGTTGGTTTTACATAATTGGAATGACAACGATTGCATGAAG 823
                                                                                                                                                                                                                                                                                          824 ATATTAGAAAATTGTAAAGAAGCTATTTCAGGTGAAAGCAAAACAGGAAAAGTAGTTGTC 883
                                                                                                                                                                                                                                                                                                                                                              685 TICTIGAAGAATIGCTATGAAGCACTACCTGCAAATGGGAAGGTGATAATAGCGGAGTGC 744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   823 GGIGGAGATATGTTTGCGAGTGTTCCGAAAGCTGATGCTATTTTTATGAAGTGGATTTGC 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATAATTGGAATGACAACGATTGCATGAAGATATTAGAAAATTGTAAAGAAGCTATTTCA 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  883 CACGÁTTGGAGTGATGÁGCACTGCTTGAAGTTTTTTGAÁGÁACTGCTÁCGAGGCACTACCA 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      854 GGTGAAAGCAAAAAGAAAAGTAGTTGTCATAGATACTGTGATAAAGGAAAACAAAGAT 913
                                                                       565 GCTCCAGCTTACCCTGGTGTCGAGCACGTTGGTGGCGACATGTTTGCCAGTGTGCCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              494 GACCCTGCATATAACAAGTCATTCAATGAGGCAATGGCTTGTGATTCTCAGATGTTGAAC
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                                                                                                                                                                                                                   625 GCAGATGCCATTTCATGAAGTGGATTTGTCATGATTGGAGCGACGAGGAGCATTGCCTAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      523 GAAGGAGGCATTCCATTTAACAAGGCTTATGGAA1GACAGCCTTTGAGTACCATGGAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cahoon, Rebecca E.
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, Antoni
APPLICANT: Shan, Jenni
APPLICANT: Shan, Jenni
TITLE OF INVENTION: Plant Caffeic acid 3-O-Methyltransferase Homologs
FILE REFRENCE: BB1327 US NA
FURENT APPLICATION UNDER: US/09/500,569
CURRENT FILING DATE: 2000-02-09
EARLIER PILING DATE: 1999-February-10
NUMBER OF SEQ ID NGS: 28
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1370;
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Pred. No. 4.1e-20;
0; Mismatches 292;
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Patent No. 6329204
GENERAL INFORMATION:
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Best Local Similarity
Matches 315; Conservat
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US-09-500-569-3
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                                                                                                                                                                                                                                                 MODIFICATION OF LIGNIN SYNTHESIS IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 230; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/204,288
FILING DATE: 10-MAR-1994
CLASSIFICATION NUMBER: US/08/204,288
FILING DATE: 10-MAR-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: B9119279.9
FILING APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/01460
FILING APPLICATION NUMBER: PCT/GB92/01460
FILING APPLICATION NUMBER: PCT/GB92/01460
FILING DATE: 09-SEP-1992
ATPONENT/AGENT INFORMATION:
ANAME: APPLICATION NUMBER: PCT/GB92/01460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REPERENCE DOCKET NUMBER: 206860/SEE36543/UST
TELEPOMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEPAX: (202) 861-3000
TELEPAX: 6714627 CUSH
TELEX: 6714627 CUSH
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P. STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20005-3518
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                     Bernard J.M.
                                                            INZE, Dirk G.
JOUDNIN, Lise
KNIGHT, MARY E.
VAN MONTAGU, MARC
LEGRAND, Michel
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EDNESS: single
                                                                                                                                                                  APPLICANT: VAN MONTANAPA APPLICANT: VAN MONTANAPA APPLICANT: LEGRAND, PITTLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1100 New CITY: Washington
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es 259; Conserv
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TOPOLOGY: line
MOLECULE TYPE: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   699 AAAAITTGTCAGGAAGCAACAATTTGACATTTGTTGGTGGGGACATGTTTAAATGCATCC 758
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                                                                                       528 CCTAIGGAAIGCAAGCATITGAGTACCAIGGCACAGATCCAAGAITCAACAAAGIGITCA
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                                                                                                                                                           519 ATGAGGCAATGGCTTGTGATTCTCAGATGTTGAACTTGGCGTTTAGAGATTGCAATTGGG
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CURRENT FILING DATE: 2000-02-09
EARLIER APPLICATION NUMBER: 60/119,587
EARLIER PILING DATE: 1999-February-10
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
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Pred. No. 9.7e-17;
0; Mismatches 191; Indels
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Patent No. 6329204
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Best Local Similarity 52.4°
Matches 210; Conservative
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ORGANISM: Glycine max
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                                                                                                                                                   994 TCTAGCTTGGCCACAAAGGTGTGGTTCACATGAGGTGTGATCATGTTGGCACATAATCCA 1053
G-----ACAATGGGAAGGTGATTGTGGCAGAATGCATTCTTCCAGTGGCTCCAGAC 993
                                                                               914 GAGCGCCAAGTTACTGAACTAAAGCTCCTTATGGATGTACACA---TGGCATGTATTATT 970
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52.9%; Pred. No. 3.8e-17;
Live 0; Mismatches 205; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KNIGHT, Mary E.
VAN MONTAGU, Marc
LEGRAND, Michel
LEGRANTION: MODIFICATION OF LIGNIN SYNTHESIS IN
NVENTION: PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: D. C.
COUNTRY: U.S.A.
ZIP: 2006-518 FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEADABLE FORM:
MARE: FLOPS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/204,288
FILING DATE: 10-MAR-1994
CLASSTERICATION NUMBER: GB 9119279.9
FILING DATE: 10-SEP-1991
PRIOR APPLICATION NUMBER: PCT/GB92/01460
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, Paul N.
REGISTRATION NUMBER: 16,773
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REFERENCE/DOCKET NUMBER: 206860/SEE36543/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                       1031 AGCTACAAAATATCTCCCT 1049
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Patent No. 5959178
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FRITIG, Bernard J.N
INZE, Dirk G.
JOUANIN, Lise
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 52.99
Matches 231, Conservative
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Pred. No. 6.3e-16;
0; Mismatches 259;
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Lignin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Materials and Methods for TITLE OF INVENTION: Materials and Methods for TITLE OF INVENTION: Modification of Plant Lighter CHRENT APPLICATION NUMBER: US/09/615,192A CURRENT APPLICATION NUMBER: US 08/75,316 FRIOR FILING DATE: 1997-11-21 FRIOR APPLICATION NUMBER: US 08/713,000 FRIOR FILING DATE: 1996-09-11 FRIOR PILING DATE: 1996-09-11 FRIOR APPLICATION NUMBER: US 09/169,789 FRIOR APPLICATION NUMBER: US 09/169,789 FRIOR FILING DATE: 1998-10-09 NUMBER OF SEQ ID MOS: 405
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 107, Application US/09615192A
Patent No. 6410718
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, 11kka
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US-09-615-192A-107
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Matches 280; Conservative
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                                                                                            GCCTCTACCTATCCTGGTGTGAGCATGTGGGAGAGATATGTTTGAAAGTGTGCACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Chiang, Vincent L
APPLICANT: Carraway, Daniel T
APPLICANT: Smeltzer, Richard H
TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
FILE REFERENCE: 50617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1380;
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                                                                                                                                                                                                                                   824 ATATTAGAAATTGTAAAGAAGCTATTTCAGGTGAAAGCAA 864
                                                 704 TIGICAGGAAGCAACAATITGACATITGITGGGGGACATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/08/991,677A
CURRENT FILING DATE: 1997-12-16
EARLIER APPLICATION NUMBER: US 60/033,381
EARLIER FILING DATE: 1996-12-16
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08991677A Patent No. 6252135 GENERAL INFORMATION:
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Best Local Similarity 50.1
Matches 325, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) NAME/KEY: CDS
; LOCATION: (67)..(1170)
US-08-991-677-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 TITGATACTIACGAGGETTITAAGGAGGTTCAGGAGTTGGTGGTGGGAGGAGGTAT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               622 IGGAATCACAGCAAAGATTATCTGTGAGGCTTTTCCTAAGCTGAAATGCATGGTGTTGGA 681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334 CATGTTTGATAGTGTACCAAGTGGCCAAGCTATTTTTATGAAGTGGATTCTGCATGATTG 393
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APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka
APPLICANT: and GRLERSON, Alastair W.
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
NUMBER OF SEQUENCES: 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score.86.2; DB 4; Length 6 Pred. No. 2.6e-14; O; Mismatches 173; Indels
Modification of Plant Lignin Content
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman STREET: 2601 Elliott Avenue, Suite 4185 CITY: Seattle
                        CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT PILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR PILING DATE: 1997-11-21
PRIOR PAPLICATION NUMBER: US 08/975,316
PRIOR PILING DATE: 1996-09-11
PRIOR PILING DATE: 1996-09-11
PRIOR PILING DATE: 1996-09-11
PRIOR PILING DATE: 1996-10-09
NUMBER OF SEQ ID NOS: 4005
SOFTWARE: PastSEQ for Windows Version 3:0
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Patent No. 5952486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.4%;
Best Local Similarity 52.3%;
Matches 190; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Pinus radiata
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 127
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                                                                                                                                                                                                                                                                   1047 GGCGGGAAAGAGAGGACACAGAAGGAGTTCGAGGCGATTGGCCAAAGGGGCCGGATTTCAG 1106
                                     914 GAGCGCCAAGTTACTGAACTAAAGCTCCTTATGGATGTACACA---TGGCCATGTATTATT 970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 GATTGGAGCGATGAAGACGCTGTGAAGATACTGAAGCGATGCAAGGAGGCCTTAGGCAAG
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Pred. No. 2.5e-15;
0; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Blokaberg, Leonard N.
APPLICANT: Blokaberg, Leonard N.
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Materials and Methods for the
FILE REFERENCE: 11000.1003c4U
CURRENT APPLICATION NUMBER: US (99/615,192A
CURRENT FILING DATE: 2000.07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1996-09-11
PRIOR FILING DATE: 1996-09-11
PRIOR FILING DATE: 1996-09-11
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
NUMBER OF SEQ ID NOS: 405
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Patent No. 6410718
GENERAL INFORMATION:
APPLICANT: Blacksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Materials and Methods for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 174, Application US/09615192A Patent No. 6410718
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Best Local Similarity 58.8
Matches 174; Conservative
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                                                                                                                                                                                                                                                                                                         502 ATATAACAAGTCATTCAATGAGGAATGGCTTGTGATTCTCAGATGTTGAACTTGGCGTT
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                                                                                                                                                                                                                                                                                                                                                                                                  562 TAGAGATIGCAATIGGGICTITGAGGGACTGGAATCCATTGTGGATGTTGGTGGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGAATCACAGCAAAGATTATCTGTGAGGCTTTTTCCTAAGCTGAAATGCATGGTGTTGGA
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                       Length 744;
                                                                                                                                                                                                                                                               173; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEGRAND, Michel
ENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
ENTION: PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
TILING DATE: 10-MAR-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                  Score 86.2; DB 4;
Pred. No. 2.7e-14;
0; Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CUSHMAN DARBY & CUSHMAN, L.L.P
                              NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSEQ for Windows Version 3.0
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Bernard J.M.
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Patent No. 5959178
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ZIP: 20005-3518
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

"MADIUMER: IBM PC COMPATIBLE
"OMPHITER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNIGHT, Mary E.
VAN MONTAGU, Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GREEL INCORPATION:
GREEL INCORPATION:
APPLICANT: VAN DOORSELAERE,
APPLICANT: FRIITG BETNARD
APPLICANT: INZE, DIRK
APPLICANT: OUDANIN, Lise
                                                                                                                                                                                                                     7.4%;
           PRIOR FILING DATE: 1998-10-09
                                                                                                                                                                                                              Query Match 7.4
Best Local Similarity 52.3
Matches 190; Conservative
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TITLE OF INVENTION: PI
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                         TYPE: DNA
ORGANISM: Pinus radiata
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                           SEQ ID NO 51
LENGTH: 744
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US-08-204-288-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.4%; Score 86.2; DB 2; Length 744; Best Local Similarity 52.3%; Pred. No. 2.7e-14; Matches 190; Conservative 0; Mismatches 173; Indels
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Patent No. 6410718
GENERAL INFORMATION:
APPLICANT: Blocksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Materials and Methods for the
FITE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003c4U
CURRENT APPLICATION NUMBER: US/09/615,192A
                                                                                      PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/713,000
FILING DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: SLEATH, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000/1003C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR PILING DATE: 1997-11-21
PRIOR PAPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
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3ER: US 08/975,316
                         US/08/975,316
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LENGTH- 744 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                           TELEFAX: 206-269-0563
TELEX:
                            APPLICATION NUMBER:
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                                              FILING DATE:
CLASSIFICATION:
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US-09-615-192A-51
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US-08-975-316-51
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PRIOR APPLICATION DATA,
APPLICATION NUMBER: GB 9119279.9
FILING DATE: 10-SEP-1991
PRIOR APPLICATION DATA;
APPLICATION NUMBER: PCT/GB92/01460
FILING DATE: 09-SEP-1992
ATTORNEY, AGENT INFORMATION:
NAME: KOKULIS, Paul N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 206860/SEE36543/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
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Db 1181 TAGATTTCTACTGTACATT 1199
Search completed: November 10, 2003, 01:53:12
Job time : 105 secs
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(without alignments)
8029.308 Million cell updates/sec
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cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

cgn2_6/ptodata/2/pubpna/US06_NBW_PUB.seq:*

cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

cgn2_6/ptodata/2/pubpna/US08_NBW_PUB.seq:*

cgn2_6/ptodata/2/pubpna/US08_NBW_PUB.seq:*

cgn2_6/ptodata/2/pubpna/US08_NBW_PUB.seq:*

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cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

cgn2_6/ptodata/2/pubpna/US09_NBW_PUB.seq:*

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cgn2_6/ptodata/2/pubpna/US09_NBW_PUB.seq:*

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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                               OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Perfect score:
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Description	Sequence 13958, A Sequence 5577, Ap	Sequence 1726, Ap Sequence 23, Appl Sequence 3502, Ap	Sequence 24, Appl Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli	Sequence 10987, A Sequence 3, Appli Sequence 13211, A	Sequence 2, Appl Sequence 25, Appl Sequence 2582, Ap Sequence 5, Appli Sequence 107, App
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SUMMARIES	US-09-878-574-13958 US-09-878-574-13958	US-U9-8/8-5/4-1/26 US-10-361-460-23 US-09-878-574-3502	US-10-361-460-24 US-09-947-027-5 US-10-091-009-5	US-09-878-574-10987 US-09-129-298-3 US-09-878-574-13211	US-10-361-460-25 US-10-361-460-25 US-09-938-842A-2582 US-09-796-256A-5 US-10-174-693-107
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US-10-174-693-1 US-10-174-693-1	US-10-174-693-51	-09-878-574	4 US-10-137-036-6	4 US-10-137-036-1	4 US-10-253-971-5	US-09-923-876-23	0 US-09-878-574-97	2 US-10-289-757-4	US-09-923-	US-09-878-574-4	US-10-174-693-1	US-10-213-473-2	US-10-174-693-1	US-10-174-693-19	-473-2	4 US-10-213-473-2	4 US-10-213-473-2	2 US-10-361-460-2	2 US-10-289-757-4	5 US-10-174-693-1	4 US-10-213-473-2	US-09-923-876-10	2 US-10-289-757-15	2 US-10-289-757-4	US-09-923-876-89	2 US-10-289-757-1	2 US-10-28
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ALIGNMENTS

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US-09-878-574-13958
) Sequence 13958, Application US/09878574
) Patent No. US20020110548A1
) GENERAL INFORMATION:
) APPLICANT: Byrum, Joseph R.
) APPLICANT: Thompson, Michael D.
) TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

CURRENT APPLICATION NUMBER: US/09/878,574

CURRENT FILING DATE: 2001-12-21
) PRIOR PILING DATE: 1999-06-14
) NUMBER OF SEQ ID NOS: 15775

LENGTH: 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701068136H1
US-09-878-574-13958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 193; Conservative
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Best Local Similarity
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81 ATTIGCTIGGCTICALAGAITCTAAGIGICTAAAATGGATGGITGAGCTIGACATACCCG 140
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                                                                                                                                                                       Length 381;
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Pred. No. 5.4e-22;
0; Mismatches 243; Indels
                                                                                                                                                                       DB 10;
                                                                                                                                                                  Score 142.2; DB 10;
Pred. No. 2.6e-28;
0; Mismatches 108;
                           LENGTH: 381
TYPE: DNA
TYPE: DNA
ORGANISM: Glycine max
COTHER INFORMATION: Clone ID: LIB3028-034-Q1-B1-D6
US-09-878-574-1726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Helentiaris, Timothy G. APPLICANT: Bowen, Benjamin A. APPLICANT: Bowen, Benjamin A. APPLICANT: Bowen, Benjamin A. APPLICANT: Bowen, Benjamin A. TITLE OF INVENTION: Genes Encoding Enzymes for TITLE OF INVENTION: Biosynthesis and Uses The FILE REFERENCE: 0709
CURRENT FILING DATE: 1997-08-27
PRIOR APPLICATION NUMBER: 60/057,082
PRIOR APPLICATION NUMBER: 60/057,082
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 85
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 23, Application US/10361460
Publication No. US20030163839A1
GENERAL INFORMATION:
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54.0%;
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Best Local Similarity 66.9%;
Matches 236; Conservative
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Best Local Similarity 54.0
Matches 292; Conservative
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US-10-361-460-23
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ORGANISM: Zea mays
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         SEQ ID NO 1726
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APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REPERBACE: 38-21 (15401) B
CURRENT APPLICATION NUMBER: US/09/878,574
PRIOR PAPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: Byrum, Joseph R.

APPLICANT: Byrum, Joseph R.

APPLICANT: Thompson, Michael D.

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21 [1540] B

CURRENT APPLICATION NUMBER: 09/933,535

PRIOR APPLICATION NUMBER: 09/333,535

PRIOR PILING DATE: 1999-06-14

NUMBER OF SEQ ID NOS: 15775

SEG ID NO 5577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          761 AAGGCTGATGCAGTTCTGCTTAAGTTGGTTTTACATAATTGGAATGACAACGATTGCATG 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 CAAGCTGATGCAGTGCTACTAAAGTGGGTTTTACATAATTGGACCGACGAAAATTGCATA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               821 AAGATATTAGAAAATTGTAAAGAAGCTATTTCAGGTGAAAGCAAAACAGGAAAAGTAGTT 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
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                                                186 GTAGAGAACTTGACAGGGACCAATAATTTGAGTTTTTGTTGGTGGTGACATGTTCAACTCT 245
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Best Local Similarity 72.1%; Pred. No. 1.5e-28;
Matches 186; Conservative 0; Mismatches 72; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Glycine max OTHER INFORMATION: Clone ID: 701097131H1
                                                                                                                                                                                                                                              Sequence 5577, Application US/09878574 Patent No. US20020110548A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 1726, Application US/09878574
; Patent No. US20020110548A1
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US-09-878-574-1726
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US-09-878-574-5577
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674 GIGITGGAACGTCCAAAIGTIGTGGAAAAITTGTCAGGAAGCAACAAITTGACAITTGTT
                                                                   187 AATTTTGATTTGCCCCAIGTCATTGAAGAIGCCCCATCTTATCCAGGAGTGGAACATGTT
                                                                                                                                             GGTGGGGACATGTTTAAATGCATCCCCAAGGCTGATGCAGTTCTGCTTAAGTTGGTTTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Genes Encoding Enzymes for Lignin TITLE OF INVENTION: Biosynthesis and Uses Thereof CURRENT APPLICATION NUMBER: US/10/361,460 CURRENT FILING DATE: 2003-02-10 PRIOR APPLICATION NUMBER: 60/057,082 PRIOR PILING DATE: 1997-08-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 12;
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Pred. No. 1.1e-19;
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 24, Application US/10361460
Publication No. US2003Q163839A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Helentjaris, Timothy G. APPLICANT: Bowen, Benjamin A. APPLICANT: Wang, Xun
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Matches 290; Conservative
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US-10-361-460-24
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US-10-361-460-24
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LENGTH: 1315
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Fatent No. US20020110549A1

GENERAL INFORMATION

APPLICANT: Byrum, Joseph R.

APPLICANT: Byrum, Joseph R.

APPLICANT: Thompson, Michael D.

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(15401)B

CURRENT APPLICATION WUMBER: US/09/878,574

CURRENT APPLICATION NUMBER: US/09/878,574

CURRENT APPLICATION NUMBER: 09/33,535

FRIOR FILING DATE: 1999-06-14

FRIOR FILING DATE: 1999-06-14

WUMBER OF SEQ ID NOS: 15775

LENGTH: 377
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9.6%; Score 111.8; DB 10; Length 377;

Best Local Similarity 56.3%; Pred. No. 4.9e-20;

Matches 209; Conservative 0; Mismatches 162; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) ORGANISM: Glycine max
) OTHER INFORMATION: Clone ID: LIB3028-009-Q1-B1-H12
US-09-878-574-3502
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US-09-878-574-3502
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us-09-868-547-3.rnpb

Db 943 GATACTTGTTGGATGCTCTGGCTCTGACACAGGCTCCCCAGGG 999 Oy 928 TGAACTAAAGGTCCTTATGGATGTACATGGATGTATTATTAATGGAAAGGAAA 987 Db 1000AGTCGTGCACGTTCATGTACATGCTGGCGCACAACCCCGGTGGGAAAGAGAGCACACCCCGTGGGAAAGAGAGACGACCTTCATGGAAGCACACCCCCGTGGGAAAGAAA	RESULT 8 US-10-091-009-5 Sequence 5, Application US/10091009 Publication No. US20020138870A1 GENERAL INFORMATION: APPLICANT: Li, Laigeng TITLE OF INVENTION: COMPOSITION, AND TITLE OF INVENTION: COMPOSITION, AND TITLE OF INVENTION: CELLULOSE CONTENT IN PLANTS FILE REFERENCE: 066040-9718 CURRENT PILING DATE: 2002-03-06 PRIOR APPLICATION NUMBER: 09/947,027 PRIOR APPLICATION NUMBER: 09/947,027 PRIOR APPLICATION NUMBER: 06/230,086 PRIOR FILING DATE: 2000-09-05 PRIOR FILING DATE: 2000-09-05 PRIOR FILING DATE: 2000-09-05 PRIOR PELING DATE: 20	FEATURE: NAME/KEY: misc feature OTHER INFORMATION: AldOW	Owery Match Best Local Similarity 49.6%; Pred. No. 3.8e-19; Matches 313; Conservative 0; Mismatches 312; Indels 6; Gaps 1; Qy 448 ATTTGAGGTCTCCTTAGGAACCTTTCTGGGACTTTATCATAAAGACCTCGATATAA 507 Db 523 ATTTAACAAGGCTTGGATTCTATATCAATAAAGACCTCAAATAA 582 Qy 508 CAAGTCTTCAACAAGGCAATGGTTGAATATCATGAACTTGAACTTCTGAAGATTCTGA 642 Qy 508 CAAGTCTTCAACAAGGCAATGGTTGAATATCATGAACTTGAACTTCTGAAGATTCTGA 642 Qy 568 TTGCAATTGAAGAGGAATGTCTGAATTCTGAACTTTGAACATGAAGAATTCTTGA 642 Qy 568 TTGCAATTGAAGAGGAATGTCTGAATTCTGAACTTTGAAGAAGATTCTTGA 642 Qy 568 TTGCAATTGGTCTTTGAAGAATCCATTTGTGAATGTTGGTGGTGGAACTGGAAT Qy 628 CACAGCAAAGATTTTTCTAACAAGAATTGTTGGTGGAACTGGAAT Db 643 GACTACAAAAGGTTTTCAAAAATTGTTGTGAAGGAATTATTGTTGGTGGAACTGGAAT Qy 628 CACAGCAAAGATTATCTGTAAGACTGAATGTTGTGGTGGAACTGCGAAT Db 703 CGTCGTTAACACCATCGTCTTAATACTTCAAAGGGCATTAACTTCGATCTCC 687
DD 979 AIRARCAGICAAACAIAAAGCATCAAGAAGTIAIGTICGAITIGIAIAIGAIGG 1038 QY 966 TIATTAAIGGAAAAGAGAAAAGAAATTGAAACTCTTCAIGGAAGCAGGT 1025 DD 1039 CCGTIAACGAGTTCAGCGTGACGAGCGAAGCCGGAT 1098 QY 1026 TCCAAAGCTACAAAATATCTCCCTTCACAGAACATCTTCGCCGAAGCCGGAT 1098 QY 1026 TCCAAAGCTACAAAATATCTCCCTTCACAGGATTTGTCTCTTAITGAGATCTATC 1082 DD 1099 TCCAAAGCTACAAAATTCTACCCGTCATTGGTGACGTCGTCGTCATCGAGGTCTATC 1168 QY 1083 CTTGAATACT 1092	RESULT 7 US-09-947-027-5 US-09-947-027-5 Sequence 5, Application US/09947027 Fatent No. US20020124281A1 GENERAL INFORMATION: FAPPLICANT: Chiang, Vincent Lee C. APPLICANT: Li, Laigeng TITLE OF INVENTION: CELULIOSE CONTENT IN PLANTS TITLE OF INVENTION: CELULIOSE CONTENT IN PLANTS TITLE OF INVENTION: CELULIOSE CONTENT IN PLANTS TITLE OF INVENTION: CELULIOSE CONTENT IN PLANTS TITLE OF INVENTION: CELULIOSE CONTENT IN PLANTS TITLE OF INVENTION: UMBER: US/09/947,027 CURRENT APPLICATION NUMBER: 00/09/947,027 CURRENT FILING DATE: 2000-09-05 PRIOR FILING DATE: 2000-09-05 PRIOR FILING DATE: 2000-09-05 SEQ ID NO 5 LENGTH: 1503 TYPE: DNA ORGANISM: aspen populus tremuloides FRAIURE: MANALVER: NAME/URE	Query Match Best Local Similarity 49.6%; Pred. No. 3.8e-19; Matches 313; Conservative 0; Mismatches 312; Indels 6; Gaps 1;	448 ATTTGAGGTCTCCTTAGGAACACCTTTCTGGGACTTTATCAATAAGACCCTGCATATAA 507 523 ATTTAACAAGGACTATGGGTGACTGCATTGATATCATGACTCTGAGATCTAGA 512 6y 508 CAAGTCTTCAAGGACTGCTTGTGATTCTCAGATGTTGACTTGAGATCTTGA 583 CAAGGTCTTCAACAAGGGAATGTCTGACACTCTTACCATTACCATGAGAAGTTCTTGA 6y 568 TTGCAATTGGTCTTTGAGGAATGTCTGACACTCTTACCATTACCATGAGAACTTGAG 6y 6y 643 GACTACAAAGGCTTTGAGGAATGTCTGACACTTGTGGATGTTGAGAACTGGAT 643 GACTACAAAGGCTTTTGAGGACTGGAATCCATTGTGGAAGTTGTTGAGACTTGAGACTGGAACTGAGACTGAGACTGGAACTGAAGACTTTGTTAGAGACTTGAGAGACTGGAACTTTGTTAGAGACTTGAGAGACTGGAACTGAACTGAACTGAAAGACTTTTACTGTGAGAACTTTACTGTAAGACTTGAAATGAATTAACAACAACATTTACAAAATGAAATAATGAAATAATGAAATAAAAAAAA

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Sequence 13211, Application US/09878574
Batent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thomson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with TITLE OF INVENTION: Plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       464 GGAACACCTTTCTGGGACTTTATCAATAAAGACCCTGCATATAACAAGTCATTCAATGAG
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                              APPLICANT: Kumar, Ramesh
APPLICANT: Kumar, Ramesh
APPLICANT: Kumar, Ramesh
APPLICANT: May, Gregory D.
TITLE OF INVENTION: The Use of Mixed Duplex Oligonucleotides
TITLE OF INVENTION: The Use of Mixed Genetic Changes in Plant.
TITLE OF INVENTION: The Use of Mixed Duplex Oligonucleotides
TITLE OF INVENTION: To Effect Localized Genetic Changes in Plant.
FILE REPERBNUE: 7991-023-999
CURRENT PAPLICATION NUMBER: US/09/129,298
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 60/054,386
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 1460
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                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 52.6
Matches 259; Conservative
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: 02/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
LENGTH: 279
                                                                                                                                                                                                                                        988 AGAAGAAGAITGGAAGAAACTCTTCATGGAAGCAGGGTTCCAAAGCTACAAAATATCTCC 1047
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883 GGCCACTGCTTAAAATTCTTGAAGAATTGCTATGACGCGTTGCCGGAAAACGGCAAGGT 942
                                                                                    218 AAAACTCGTCAGGTGCAGAGCCTCATGCGTTATCTAGCACACAATGGATTCTTTGAGATA 277
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                                                                                                                                     943 GATACTIGITGAGIGCAITCTICCCGIGGCICCTGACACAAGCCTIGCCACCAAGGG---
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CTHER INFORMATION: Clone ID: 701063901H1
US-09-878-574-10987
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Patent No. US20020110548A1
GENERAL INFORMATION:
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Publication No. US20030196218A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                    AAAATTTGTCAGGAAGCAACAATTTGACATTTGTTGGTGGGGACATGTTAAATGCATCC
                                                       ACCGTGGAATGTCTGATCACTCCACTATGTCAATGAAGAAGATTCTTGAGGACTACAAAG
                                                                                                      579 ICTITGAGGGACTGGAATCCAITGTGGATGTTGGTGGTGGAACTGGAATCACAGCAAAGA
                                                                                                                                                  648 GATTIGAAGGCCTAAAITCCATTGTTGATGTTGGTGGAGGGAACGGGTGCTACTGTTAACA
                                                                                                                                                                                              TTATCTGTGAGGCTTTTCCTAAGCTGAAATGCATGGTGGTTGGAACGTCCAAATGTTGTGG
                                                                                                                                                                                                                                        708 TGATTGTCTCTAAATATCCCTCTATTAAGGGCATTAACTTTGATTTGCCACATGTAATTG
                                                                                                                                                                                                                                                                                                                             768 GAGATGCTCCAACTTACCCCGGTGTCGAGCACGTTGGTGGCGACATGTTTGCTAGTGTG
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APPLICANT: Bowen, Benjamin A.
APPLICANT: Bowen, Benjamin A.
APPLICANT: Bowen, Benjamin A.
TITLE OF INVENTION: Genes Encoding Enzymes for Lignin
TITLE OF INVENTION: Biosynthesis and Uses Thereof
FILE REPREBRICE: 0709
CURRENT APPLICATION NUMBER: US/10/361,460
CURRENT PILING DATE: 2003-02-10
FRIOR PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 85
SOSTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 12;
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Pred. No. 2.3e-18;
0; Mismatches 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 25, Application US/10361460; Publication No. US20030163839A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     879 TTGTCATAGATACTGTG 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               948 AGTGCATACTTCCAGAG 964
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Best Local Similarity 51.3%;
Matches 273; Conservative
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; LOCATION: (57)...(1154)
US-10-361-460-25
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US-10-361-460-25
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LENGTH: 1306
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APPLICANT: Arnteen, Charles
APPLICANT: Kipp, Peter B.
APPLICANT: Kumar, Ramesh
APPLICANT: May, Gregory D.
TITLE OF INVENTION: The Use of Mixed Duplex Oligonucleotides
TITLE OF INVENTION: to Effect Localized Genetic Changes in Plants
FILE REPERENCE: 7991-023-99
CURRENT APPLICATION NUMBER: US/09/129,298
CURRENT FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 60/054,386
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 5.6e-19;
0; Mismatches 79;
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                                                                                                                                                                                                                                                                                                                                                                                       CATTAAACAATGGCCGTAAAGCAAGTGAGATTT
FILE REFERENCE; 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 13211
LENGTH: 272
                                                                                                                                                                                TYPE: DNA

: ORGANISM: Glycine max

: OTHER INFORMATION: Clone ID: 701066773H1

US-09-878-574-13211
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Publication No. US20030196218A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.8 Matches 171; Conservative
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NAME/KEY: CDS
TOTALON: (59)...(1153)
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Best Local Similarity
Matches 231; Conserv
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US-09-129-298-4
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813 ATTGCATGAAGATATTAGAAAATTGTAAAGCTATTTTCAGGTGAAAGCAAAACAGGAA 872
                                                                                854 ATTGCATAAAGATATTGAAGAATTGCAAAGAAGCGGTCCCTCCAAATATCGGAAAAGTGT 913
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Parent No. U320020078477A1
GRNERAL INFORMATION:
APPLICANT: Chiang, Vincent L
APPLICANT: Carraway, Daniel T
APPLICANT: Smeltzer, Richard H
TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
TITLE SPERRANCE: 50617/c-3532.0
CURRENT APPLICATION UNDER: US/09/796,256A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1380;
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Pred. No. 4.9e-15;
0; Mismatches 309;
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PRIOR FILING DATE: 1996-12-16
PRIOR APPLICATION WUMBER: 08/991677
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIN Ver. 2.1
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ORGANISM: Liquidambar styraciflua
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ilarity 50.1%;
Conservative (
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Best Local Similarity
Matches 325; Conserv
                                                                                                                              873 AAGTAGTTG
                                                                                                                                                                                                                                                  RESULT 15
US-09-796-256A-5
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Sequence 2582, Application US/09938842A

Patent No. US20020160378A1

GARBRAL INFORMATION:

APPLICANT: Harper, Joef

APPLICANT: APPLICANT: ALM, Tong

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

FILE REFERENCE: SCRIP1300-3

CURRENT APPLICATION NUMBER: US 60/227, 866

PRIOR APPLICATION NUMBER: US 60/227, 866

PRIOR PLING DATE: 2001-08-24

PRIOR PLING DATE: 2001-01-16

PRIOR PLING DATE: 2001-01-16

PRIOR PLING DATE: 2001-06-25

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 2582

LENGTH: 1149
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                                                                                                                                                877 AGTIGICATAGATACIGIGATAAAGGAAAACAAAGAIGAGCGCCAAGTIACIGAACIAAA
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Pred. No. 1.3e-16;
0; Mismatches 158; Indels
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity 56.4%;
Matches 208; Conservative
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Search completed: November 10, 2003, 03:17:19 Job time : 463 secs

42.5 494 9 AISO7864 39.3 852 10 BGS88377 38.2 822 10 BG643368 37.9 569 12 BM188258 37.7 606 12 BM177364 36.0 788 13 BQ166419 35.6 693 14 CA921971	35.3 826 13 BQ165418 34.9 625 9 AW733746 34.2 775 13 BQ165420 34.2 774 9 AW559420 33.7 742 9 AW567810 33.4 408 13 BU765089 33.3 420 10 BE021456 32.7 718 13 BU01459	3.4 512 10 BG509454 30.5 519 10 BG509170 30.1 668 13 BQ156708 30.1 663 12 BM528698 29.1 563 12 BM528698 28.5 639 10 BE999705 28.4 643 10 BF648180	31.0 27.2 8.2 32.7 34.7 34.7 34.7 34.7 34.7 34.7 34.7 34	ALIGNMENTS AW350290 GW210006A10D3 Gm-r1021 Glycine max cDNA clone mRNA sequence. AW350290 AW350290 AW350290 GST. Glycine max (soybean) Glycine max (soybean) Glycine max (soybean) Glycine max (soybean)	Spermatophy, eurosids divine. E 1 (bases 1 1 (bases 1 2 Vodini, L., Erpelding, J. A Functions, J. A Functions, J. A Functions, J. A Functions, J. A Functions, J. A Functions, J. A Functions, J. A Functions, J. A Functions, J. A Genomics University Edwin R. Matter (217)
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: November 9, 2003, 23:36:19; Search time 2914 Seconds	(Without alignments) 9675.083 Million cell updates/sec Perfect score: 1160 Sequence: 1 gttgctattatggcttcttataaaagttatctttgtgtt 1160 Scoring table: IDENTITY NUC Gapop 10.0, Gapext 1.0	Searched: 22781392 segs, 12152238056 residues Total number of hits satisfying chosen parameters: 45562784 Minimum DB seg length: 0 Maximum DB seg length: 0 Post-processing: Minimum Match 08 Maximum Match 08 Maximum Match 08	sting first em_estba em_esttin em_esttin em_esttin em_esttin em_esttin gd_estti gd_estti		28: gp_gss1:* 29: gp_gss2:* 29: gp_gss2:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES Result No. Score Match Length DB ID C 1 660.4 56.9 697 9 AW350290 C 1 660.4 56.9 697 9 AW350290 C 1 860.4 56.9 697 9 AW350290 C 1 860.4 56.9 697 9 AW350290 C 1 860.4 56.9 697 9 BM523459 C 1 860.4 56.9 697 9 BM523459 C 1 860.4 56.9 697 9 BM523459 C 2 588 50.7 589 12 BM523459 C 3 557.8 48.1 561 13 BQ452916 C BI245401 FISIC9 Fo

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Reracking was performed by Genome Systems, St. Louis,
http://www.genomesystems.com, and sequencing by the Keck
Center for Caparative and Functional Genomics,
University of Illinois,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             day old 'Williams' seedlings which were propagated on paper towels with distilled water. Stratagene's CDNA paper towels with distilled water. Stratagene's CDNA Synthesize Kit (acatalog #200401) was used to synthesize the CDNA. The Gm-c1004 library was constructed by Dr. Paul Keim & Virginia H. Coryell, Department of Biology, exail: paul keimen Arizona University, Flagstaff, Az 8601 cemail: paul keimenedu, virginia.coryell@nau.edu. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Computational Biology
                                                                                                                                                                                                                                                                                                                                                                                    697 AGTATTTGAMMNNCNTTAGGAA-NNNNNNNGGGACNNNNNCNNTMAAGACCCTGCATA 639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         565 AGATTGCAATTGGGTCTTTGAGGGACTGGAATCCATTGTGGATGTTGGTGGTGGTGGAACTGG 624
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                  This clone is available through: Genome Systems, Inc. 4633 World parkway Circle 87. Louis, Missouri 63134. Por further information call: (800) 430-0030 or (314) 427-3222 PAX:(888)919-3324 or (314) 427-3324 or contact:clones@genomesystems.com or info@genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        625 AATCACAGCAAAGATTATCTGTGAGGCTTTTCCTAAGCTGAAATGCATGGTGTTTGGAACG
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157 c 97 g 221 t 24 others
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                                                                                                                    ystems.com web site:www.genomesystems.com Seq primer: 5'-TTTTTTTTTTTTTTTTTT(A/C/G)-3'.
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0; Mismatches 25;
                                                                                                                                                                                                                        'organism="Glycine max"
                                                                                                                                                                                                                                                                                               /db_xref="taxon:3847"
/clone="Gm-r1021-2837"
                                                                                                                                                                                                                                                                                                                                                                       'lab_host="XL10-Gold"
                                                                                                                                                                                                                                                'mol_type="mRNA"
'cultivar="Williams"
                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                  'tissue_type="root"
1-vodkin@uiuc.edu
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sam84409.y2 Gm-c1087 Glycine max cDNA clone SOYBRAN CLONE ID:
Gm-c1087-426 5' similar to TR:022555 022555 O-METHYTRANSPERASE. [2]
TR:023308 ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, At. 35801 For further information
call: (800)-5314363 or contact: ccu@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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                                                                                                                                                                                                                                                                                           985 AAAAGAAGAAGATTGGAAGAAACTCTTCATGGAAGCAGGGTTCCAAAGCTACAAAATATC 1044
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/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The mRNA was prepared using polyafract mRNA system
from PROMEGA. The cDNA was prepared using the STRATAGENE
kit. Complementary DNA was synthesized from mRNA using a
primer consisting of a poly(dT) sequence with a XhoI
                                                                                                                                                                                                                    159
924
                                                                                                                                             984
                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 TCCCTTCACAGGATALTTGICTCTTALTGAGATCTATCCTTGAATACTGACGCTGCAATA 39
                                                                      278 AACAGGAAAAGTAGTTGTCATAGATACTGTGATAAACGAAAACAAAGATGAGCGCCAAGT
                                                                                                                                             925 TACTGAACTAAAGCTCCTTATGGATGTACACATGGCATGTATTATTAATGGAAAAGAGAG
                                                                                                                                                                                                                    218 TACTGAACTAAAGCTCCTTATGGATGTACACATGGCATGTATTATTAATGGAAAAGAGAG
                                                                                                                                                                                                                                                                                                                                                              158 AAAAGAAGATTGGAAGAACTCTTCATGGAAGCAGGGTTCCAAAGCTACAAATATC
865 AACAGGAAAAGTAGTTGTCATAGATACTGTGATAAACGAAAACAAAGATGAGCGCCAAGT
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Public Soybean BST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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/bol_type="mkp"
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/clore="SOYBEAN CLONE ID: Gm-c1087-426"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1105 TICCATTTAGTAGTTAATTTGCATGTTATCAATAAAAT 1142
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High quality sequence stop: 438.
Location/Qualifiers
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Fax: 314 286 1810
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Fax: 314 286 1810
Email: est@watson.wstl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact: ccu@resgen.com web site:
             Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
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/clone="SOYBEAN CLONE ID: Gm-c1081-3159"
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/lab_host="DH108"
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Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
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/organism="Glycine max"
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High quality sequence stop: 449.
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                             BookI adapters (5'0H-AATTCGGCACGAG and 3'GCCGTGCTCP) were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The CDNA fragments were directionally cloned into the EcoRI-XhoI restriction sites of the pBluescript vector. The vector was previously dephosphorylated. The ligated cDNA fragments were transformed into DH10B by electroporation. Library is in LB medium with ampicillin and glycerol 3. Average insert size: 800 bp."
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EST.
Glycine max {soybean}
Glycine max
Glycine max
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Agnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae, Papilionoideae, Phaseoleae;
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GTCAATTCTACAAGTCCCACCAACTAAAACTCGTCAGGTCCAGAGCCTCATGCGTTATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 AGCACACAATGGATTCTTTGAGATAGTAAGAATCCATGACAACATAGAAGCATATGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAAGATCTCACAGTATTTGAGGTCTCCTTAGGAACACCTTTCTGGGACTTTATCAATAA
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                                                                                                                                                                                                                                                                                                                                                                                       Length 589;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                    Score 588; DB 12;
Pred. No. 1.8e-117;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                    50.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 561)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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Best Local Simil
Matches 588; C
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673

421

733

LOCUS

RESULT 3 BQ452916

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE

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/note="Torgan: Root: Vector: pGEM; Forrest roots were inoculated with Fusarium solani f. sp. glycinae and samples were collected after 14 days of inoculation. Total RNA was used for CDNA synthesis using SMART PCR CDNA Synthesis kit (CLONTECH, CA). CLONTECH PCR.Select Subtraction system was used to enrich rare transcripts expressed in Forrest roots under inoculation by F. solani and cloned in pGEM vector. ESTS were sequenced using M13 universal forward or reverse primer."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AISO7864.1 GI:4405715
BST.
Glycine max
Glycine max
Glycine displantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300
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sa88b04.y1 Gm-c1004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: GGm-c1004-6344 5' similar to TR:022308 022308 7-O-METHYLTRANSFERASE.
[3] TR:022309 TR:022555 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                               120
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               lib="Forrest infected Subtraction Library"
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                                                                                                                                                                                                                                                              Length 573;
                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                          core 548; DB 12;
Pred. No. 9e-109;
                                                                                                                                                                                                                                            47.2%; Scc. No. ... 100.0%; Pred. No. ... 0; Mismatches
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 548; Conservative
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ORGANISM
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ORIGIN
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VERSION
KEYWORDS
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AI507864
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eudicots; rosids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Ignal MJ and Lightfoot, DA Center of Excellence in Soybean Research, Teaching and Outreach Southern Illinois University at Carbondale Room 176, Ag. Building, Mail Code 4415, Carbondale, IL 62901-4415,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 573)
Idbal,M.J. and Lightfoot,D.A.
Differentially expressed mRNA sequences identified by subtraction hybridization from soybean, Glycine max (L.) Merr. var. Forrest, roots in response to Fusarium solani f. sp. glycinae inoculation Unpublished
AATCACAGCAAAGATTATCTGTGAGGCTTTTCCTAAGCTGAAATGCATGGTGTTGGAACG
                           AATCACAGCAAAGATTATCTGTGAGGCTTTTCCTAAGCTGAAATGCATGGTGTTGGAACG
                                                                                                                                                                                                                                                              TGACAACGATTGCATGAAGATATTAGAAAATTGTAAAGAAGCTATTTCAGGTGAAAGCAA
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                                                                                                 GTTTAAATGCATCCCCAAGGCTGATGCAGTTCTGCTTAAGTTGGTTTTACATAATTGGAA
                                                                                                                                                                                        GTTTAAATGCTTTCCCAAGGCTGATGCAGTTCTGCTTAAGTTGCTTTACATAATTGGAA
                                                                                                                                                                                                                             TGACAACGATTGCATGAAGATATTAGAAAATTGTAAAGAAGCTATTTCAGGTGAAAGCAA
                                                                                                                                                                                                                                                                                                                                         AACAGGAAAAGTAGTTGTCATAGATACTGTGATAAACGAAAACAAAGATGAGCGCCAAGT
                                                                                                                                                                                                                                                                                                                                                                                TACTGAACTAAAGCTCCTTATGGATGTACACATGGCATGTATTATTAATGGAAAAGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAAGAAGAAGAAGAAACTCTTCATGGAAGCAGGGTTCCAAAGCTACAAAATATC
                                                                              TCCAAATGTTGTGGAAAATTTGTCAGGAAGCAACAATTTGACATTTGTTGGTGGGGACAT
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
___eurosids I; Fabales, Fabaceae, Papilionoideae, Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/cultivar="Forrest"
/db_xref="taxon:3847"
/dev_stage="14 days after inoculation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 618 453-3121
Fax: 618 453-7457
Email: mjiqbal@siu.edu, ga4082@siu.edu
Seg primer: M13 Forward.

    .573
    organism="Glycine max"

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BI245401.1
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ORGANISM
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TITLE
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BI245401
LOCUS
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KEYWORDS
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180

191

253

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Medicago.

1 (bases 1 to 852)

Harrison, M.J., Liu,J., Town,C.D., Van Aken,S., Utterback,T., Cho,J.

and Fraser,C.M.

ESTs from phosphate-starved roots of Medicago truncatula, 2001
Unpublished
Contact: Harrison M.J.
Contact: Harrison M.J.
Contact: Harrison M.J.
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
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Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                         TAGCACACAATGGATTCTTTGAGATAGTAAGAATCCATGACAACATAGAAGCATATGCTC 300
                                                                                                                                                                                                                                                                                                                                      TAGCACACAATGGATTCTTTGAGATAGTAAGAATCCATGACAACATAGAAGCATATGCTC 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 TCACTGCTTCAGAGTTACTTGTCAAAAGCAGTGAGCTTAGTTTAGCTCCAATGGTTG 360
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EST490186 MHRP- Medicago truncatula cDNA clone pMHRP-53C11, mRNA
           TCACTGCTGCTTCAGAGTTACTTGTCAAAAGCAGTGAGCTTAGTTTAGCTCCAATGGTTG
                                                                                                        ACATACCCGACATAATCCACAGCCATAGCCATGGCCAACCCCATTACTTTTTAGGTTTGG
                                                                                                                                                                                                                    TGTCAATTCTACAAGTCCCACCAACTAAAACTCGTCAGGTGCAGAGCCTCATGCGTTATC
                                                                                                                                                                                                                                                                                TGTCAATTCTACAAGTCCCAACTAAAACTCGTCAGGGTGCAGAGCCTCATGCGTTATC
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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
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Medicago truncatula
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheo;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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/organism="Medicago truncatula"
/oul_type="mRNA"
/oul_tivar="A17"
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/lab_host="XLOLR"
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/clone="pMHRP-53C11"
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Fax: 580-221-7380
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                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1800
Exa: 314 286 1810
Exa: 314 286 1810
Exa: 314 286 1810
Exail: estewatson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4353 or contact via email: ccu@resgen.com
Insert Length: 1307 5td Exror: 0.00
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                                                                                                                                                                                                                                Unpublished
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="GENOME SYSTEMS CLONE ID: Gm-c1004-6344"
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Pred. No. 8.1e-97;
0; Mismatches 1; Indels
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/mol_type="mRNA"
/db_xref="taxon:3847"
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High quality sequence stop: 393
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Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                               822 bp mRNA linear · EST 24-APR-2001 KV3 Medicago truncatula cDNA clone pKV3-46C11 5' end,
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/clone_lib="KV3"
/note="Vector: pBluescript SK -; Site_l: EcoRI; Site_2:
/note="Vector: pBluescript SR or polyA+ enriched RNA. The CDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
Stratagene. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
a 124 c 169 g 279 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /moi_type="mRNA"">
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/cultivar="denotype A17"
/db xef="lexxon:3880"
/clone="pKV3-46C11"
/tissus_type="Seedling roots"
/dev_stage="3 days post-inoculation with Sinorhizobium meliloti"
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ESTs from roots of Medicago truncatula 72 h after Rhizobium inoculation, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
Contact: VandenBosch K
Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M393775E TIGR Sequence name: MTECA18TK More information available at: www.medicago.org Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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Pred. No. 8.3e-86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: kvandenb@cbs.umn.edu
                                                                                                                                                                                                        BG645368.1 GI:13780480
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                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 822)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 612 624 2755
Fax: 612 625 1738
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Nhol; At the trifoliate Stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this period, they were fertilized twice weekly with 1/2 Hoadlands solutions containing 20um potassium phosphate. cDNA was prepared from polyA+ enriched RNA. The CDNA was directionally ligated into the Unizap XR vector from Strateagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing phase using Ex-assist helper phage and propagated in
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                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                                                            Score 456.2; DB 10; Length 852;
Pred. No. 9.2e-89;
0; Mismatches 203; Indels 15;
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/close 112= "Gm-c1074"
//note="Vector: pBluescript II SK+; Site 1: ECORI; Site 2: XhoI; The CDNA library was constructed from mRNA isolated from mRNA isolated from mRNA isolated from mRNA isolated from mRNA isolated from mRNA isolated from mRNA isolated from mRNA isolated from mRNA isolated from mRNA isolated from mRNA isolated from mRNA isolated from mRNA isolated from mRNA plant tissue (axpanded average with Pseudomonas syringae pv. 4) 4, 8, 12, 24, 36, and 53 hrs after inoculation and their mRNA pooled equally for cDNA construction. The library was prepared using the Stratagene pBluescript II SK(+) library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with an XhoI restriction site. EcoRI adaptors were ligated to the blunt ended cDNA fragments followed by XhoI digestion. The cDNA insert is protected from XhoI digestion via methylation during first strand synthesis. The CDNA fragments were directionally cloned into the ECORI-XhoI restriction site of the
South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact: ccu@resgen.com web site: www.resgen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 425.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pBluescript vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DH10B host cells. Plant care, inoculations, and library construction were performed by Steve Clough (Lila Vodkin lab, University of Illinois)."
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                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:3847"
/clone="SOYBRAN CIONE ID: Gm-c1074-4849"
/tissue_type="seedlings induced for HR (hypersensitive
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37.9%; Score 439.2; DB 12; Length
al Similarity 86.7%; Pred. No. 4.2e-85;
496; Conservative 0; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="9-11 day old"
/lab_host="DH10B"
                                                                                                                                                                                                                                  organism="Glycine max"
                                                                                                                                                                           Location/Qualifiers
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(dases 1 to 569)

Shoemaker, K., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna Shoemaker, K., Keim, P., Vodkin, L., Kucaba, T., Martin, J., Beck, C., A., B. Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Bock, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
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consisting of a poly(dT) sequence with an XhoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA insert is protected from KhoI digestion via methylation during first strand synthesis. The cDNA fragments were directionally closed into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DHIOB host cells. Plant performed by Steve Clough (Lila Vodkin lab, University of Illinois)."
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Public Soybean EST Project
Rashington University School of Medicine
1444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
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Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BM177364 60-bbC-2001 saj80d09.y1 Gm-c1074 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1074-2873 5' similar to TR:022555 022555 0-METHYTRANSFERASE. [2
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1...comlsm="Glycine max"
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-cl074-2873"
/tissue type="seedlings induced for HR (hypersensitive response)"
                                                                                          CCAAGATTATCTGTGAAGCATTTCCTGACTTGAAATGCATTGTGTTTGACGTCCGCAGG
                                                                                                                                                                                                                     478 ITGTGGAGAACTTGTCAGGAAGCAACAATTTGACATATGTTGGAGGGGACATGTTCAAAT
                            CAAAGATTATCTGTGAGGCTTTTCCTAAGCTGAAATGCATGGTGTTGGAACGTCCAAATG
                                                                                                                                                                      TTGTGGAAAATTTGTCAGGAAGCAACAATTTGACATTTGTTGGTGGGGACATGTTAAAT
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High quality sequence stop: 4
Location/Qualifiers
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BM177364.1 GI:17400582
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Glycine max
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COMMENT

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EST 09-MAY-2003
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/note="Vector: pBluescript SK-; Site_l: EcoR1; Site_2:
Xhol; cDNA was prepared from polyA+ enriched RNA. The cDNA
                 512
                                                                                                                                                                                            632
                                                                                                                                                                                                              ATTITGETTIGATGGATTGGAATCAATTGTGGATGTTGGTGGTGGAAATGGAACCACTG 605
                                                                                                                                                                                                                                                                                                            GTAAAATTATTIGIGAGACTTTICCTAAGTIGAATGTATTGTGTTIGATAGGCCACAAG 665
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosid
; eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
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VandenBosch, K., Endre, G., Silverstein, K, Town, C.D., Van Aken, S., Utterback, T., Cheung, F. and Praser, C.M.
The Medicago truncatula 6K unigene set: cDNA clones selected and re-arrayed from various libraries
                                                                                                                                         CATITIAAIGAIGCAAIGGCIAGIGAIICIAAAIIGAAAACIIGGCAIIGAGAIIGIG
                                                                                                                                                                                                                                                                         CAAAGATTATCTGTGAGGCTTTTCCTAAGCTGAAATGCATGGTGTTGGAACGTCCAAATG
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           453 AGGICTCCTTAGGAACACCTTTCTGGGACTTTATCAATAAAGACCCTGCATATAACAAGT
                                                        GTGTTACTTTAGGGTCTGGTTTTTGGGATTTTTCTTGATAAAATCCTGAATATAATAGAT
                                                                                                CATTCAATGAGGCAATGGCTTGTGATTCTCAGATGTTGAACTTGGGCGTTTAGAGATTGCA
                                                                                                                                                                                     ATTGGGTCTTTGAGGGACTGGAATCCATTGTGGATGTTGGTGGTGGAACTGGAATCACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CA921971 693 bp mRNA linear EST 09-MAY.
EST639689 MTUS Medicago truncatula cDNA clone MTUS-46H12, mRNA
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University of Minnesota
20 BioSci Center, 1445 Gortner Ave, St. Paul, MN 5510
Tel: 612 624 2755
Fax: 612 625 1738
Email: kvandenbecbs.umn.edu
Alias Clone pDSIR-19116
TIGR sequence name: MTUBTSGTV
More information is available at: www.medicago.org
Seq primer: (gtA AtA CgA CtC Act AtA ggg C).
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/mol_type="mRNA"
/cultivar="A17"
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/dev_stage="various stages"
/lab_host="XLOLR"
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/clone="MTUS-46H12"
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Contact: VandenBosch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGATAGTAAGAATCCATGACAACATAGAAGCATATGCTCTCACTGCTTCAGAGTTAC 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trefragageracidarcifrefritageaceaarderreagrererrearceaacre 365
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                                                                                     [Dases 1 to 788]
VandenBosch,K., Endre,G., Silverstein,K, Town,C.D., Van Aken,S., Utterback,T., Cheung,F. and Fraser,C.M.
The Medicago truncatula 'Kiloclone' set, ESTs selected and Tre-arrayed from various libraries
Unpublished
                                                                                                                                                                                                                                                                                                                                            Email: kvandenb@cbs.umn.edu
TIGR sequence name: MTNAIO5TK Alias Clone name:DSIR-19L16 More
information is available at: www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
1. 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 CAACTAAAAACTCGTCAGGTGCAGAGCCTCATGCGTTATCTAGCACAAAAGGATTCTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 36.0%; Score 417.8; DB 13; Length 788; Best Local Similarity 73.7%; Pred. No. 2e-80; Matches 577; Conservative 0; Mismatches 192; Indels 14;
                                                                                                                                                                                                                                                                                           Ž
                                                                                                                                                                                                                                                                                      St. Paul,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="A17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="mixed tissues"
                                                                                                                                                                                                                     Contact: VandenBosch K
Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave,
Tel: 612 624 2755
Fax: 612 625 1738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="various stages"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:3880"
/clone="pKVKC-9A5"
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/done libe "Gm-c1072"
//note="Wector: pBluescript II SK+; Site I: EcoRI; Site 2:
Xhoi; The CDNA library was constructed from mRNA isolated
from 2-3 week old seedlings that were induced for symptoms
of SDS (Sudden Death Syndrome) disease by the
translocation of culture filtrate of Fusarium solani f.
Sp. glycines (Plant Cell Report 18:375-380). Cultivar PI
567374 is partially resistant to the disease SDS. Plant
tissue (expanded leaves, folded leaves, and new shoots)
were collected at 1, 6, 24, and 48 hrs. after incculation
and their mRNA pooled equally for cDNA construction. The
library was prepared using the Stratagene pBluescript II
SK(+) library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with an XhoI restriction site. BookI
adaptors were ligated to the blunt ended cDNA fragments
followed by XhoI digestion. The cDNA insert is protected
from XhoI digestion via methylation during first strand
synthesis. The cDNA fragments were directionally cloned
into the EcoRI-XhoI restriction site of the pBluescript
vector. The ligated cDNA fragments were inculated
by Shnxian Li (Glen Hartman lab, University of Illinois).
Library was constructed by Steve Clough (Lila Vodkin lab,
University of Illinois)."
                                                                                        1 (bases 1 to 546)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kacaba,T., Martin,G., Beck,C., Whylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Sohurk,R., Kitter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 CAGAGCCTCATGCGTTATCTAGCACACAATGGATTCTTTGAGATAGTAACAATCCATGAC 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 ATTACTTTTCAGAGTTGGTGTCTACAAGTCCCACCAACTAAAACTCGTCAGGTG
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                        eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDS
                     ophyta; eudicotyledons; core eudicots;
Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             οĘ
                                                                                                                                                                                                                                                                                                                                                                                                             Louis, MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1072-4190"
/clasue type="seedlings induced for symptoms"
(Sudden Death Syndrome) disease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 546;
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                                                                                                                                                                                                                                                                                                                          Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 413; DB 12;
Pred. No. 2.1e-79;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="2-3 weeks old"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 www.resgen.com
Seg primer: -40RP from Gibco
High quality sequence stop: 421.
Location/Qualifiers
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/organism≂"Glycine max"
                  Spermatophyta; Magnoliophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
                                             eurosids I; Fabales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
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ses 471; Conservative
                                                                                                                                                                                                                                                                                                    Unpublished
                                                                     Glycine
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Matches
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AUTHORS
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was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1074 AGATCTATCCTTGAATACTGACGCTGCAATATTCCATTTAGTAGTTAATTTGCATGTTAT 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             saj59h07.yl Gm-c1072 Glycine max cDNA linear EST 06-DEC-2001 Gm-c1072-4190 5' similar to TR:022555 022555 0-METHYTRANSPERASE. [2] TR:022308 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                014 IGGAAGCAGGGTTCCAAAGCTACAAATATCTCCCTTCACAGGATATTTGTCTCTTATTG 1073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTGTAAAGAAGCTATTTCAGGTGAAAGCAAAACAGGAAAAGTAGTTGTCATAGATACTG 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BM178815.1 GI:17402033
BST.
Glycine max (soybean)
Glycine max
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCAATAATTTGACTTATGTTGGTGGGGACATGTTCACATCTATTCCTAATGCTGATGCAG 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCTGCTTAAGTTGGTTTTACATAATTGGAATGACAACGATTGCATGAAGATATTAGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAGAAGCTGGTTTCCAAGACTATAAGATATCTCCTTTGACTGGATTTTTGTCTCTTATTG
                                                                                                                                                                                                                                                                       ω
,
                                                                                                                                                                                                                    Length 693;
                                                                                                                                                                                                                                                                 0; Mismatches 147; Indels
                                                                                                                                                                                                                 DB 14;
                                                                                                                                                                                                              Score 415.8; DB 1.
Pred. No. 5.4e-80;
                                                                                                                                                                                                              35.8%;
                                                                                                                                                                                                                                                                 Conservative
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/dev_stage="various stages"
/lab/host="XtOLR"
/clone_lib="KVKC"
/clone_lib="KVKC"
/note="Vector: Bluescript SK-; Site_l: EcoRI; Site_2:
Xhol; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTAACAATTTGACATTATGTCGGTGGGGGACATGTTCATATCTTGTTCCTAAAGCTGAT 802
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University of Minnesota
220 BloSci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
Tel: 612 624 2755
Fax: 612 624 2755
Fax: 612 625 1738
Email: kvandenb@cbe.umn.edu
TIGR sequence name: MTNAI04TK Alias Clone name:DSIR-19C17 More
information is available at: www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
                                          AACATAGAAGCATATGCTCTCACTGCTTCAGAGTTACTTGTCAAAAGCAGTGAGCTT
                                                                                                                                                                                             TTGAAGAGGTGGGTTCATGAGGAAGATCTCACAGTATTTGAGGTCTCCTTAGGAACACCT
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
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Utterback, T., Cheung, F. and Fraser, C.M.
The Medicago truncatula 'kiloclone' set; ESTs selected
re-arrayed from various libraries
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/tissue_type="mixed tissues"
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Medicago truncatula
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65 TCATTCAATGAGGCAATGGCTAGAGATTCTCAAATGAGTAATTTGGCATTGAGAGATTGC 124
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Xhol; This cDNA library was constructed from mRNA isolated
from immature flowers of field grown plants. The cDNA
library was prepared using the Stratagene pBluescript II
XR library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a poly
(dT) sequence with a Xhol restriction site. EcoRI adapters
were ligated to the blunt-ended cDNA fragments followed by
Xhol digestion. The cDNA fragments were directionally
cloned into the EcoRI-Xhol restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into XL10-Gold host cells. This library was
constructed by Dr. Randy Shoemaker and Dr. John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu.
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4353 or contact via email: ccu@resgen.com
Seg primer: -40RP from Gibco
High quality sequence stop: 411.
                                                                                                                                                                                                                                                                                                                                                                                     Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna Shoemaker, R., Keim, P., Vodkin, L., Kroaba, T., Martin, J., Beck, C., A., Bollah, B., Marra, M., Hillier, L., Kroaba, T., Mattin, J., Bowers, Y., Underwood, K., Steptoe, M., Thoising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harrey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Milson, R.
                                                                                                                                                                                                                                                                                           Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
                                                                       AW733746 mRNA linear EST 03-DEC-2001 SY7110.9.1 Gm-c1016 Glycine max CDNA clone GENOME SYSTEMS CLONE ID: Gm-c1016-10148 5' similar to TR:022309 022309 7-O-METHYLIRANSFERASE.; mRNA sequence.
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/clone="GENOME SYSTEMS CLONE ID: Gm-c1016-10148"
/tissue_type="immature flowers of field grown plants"
/clone_lib="Gm-c1016"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Mashington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Fax: 314 286 1810
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Spermatophyta; Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
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572 AATTGGGTCTTTGAGGGACTGGAATCCATTGTGGATGTTGGTGGGAACTGGAATCACA 631
                                                                            125 AAGTIGGIGTTTTGAGGGACTGGAATCCATTGTGGATGTTGGTGGTGGAACTGGAGCCACT 184
                                                                                                                                                        GCAAAGATTATCTGTGAGGCTTTTCCTAAGCTGAAATGCATGGTGTTGGAACGTCCAAAT 691
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VandenBosch, K., Endre, G., Silverstein, K., Town, C.D., Van Aken, S., Utterback, T., Cheung, F. and Fraser, C.M.
The Medicago truncatula 'Kiloclone' set; ESTs selected and re-arrayed from various libraries
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Location/Qualifiers
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ST611277 KVKC Medicago truncatula cDNA clone pKVKC-9A5, mRNA
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University of Minnesota
220 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
Tel: 612 624 2755
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Email: kvandenb@cbs.umn.edu
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/db xref="axon:3880"
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Search completed: November 10, 2003, 01:51:24 Job time : 2919 secs